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(54) Title: A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE (57) Abstract <p>Cells are genetically modified to express a luminophore, e.g., a modified (F64L, S65T, Y66H) Green Fluorescent Protein (GFP, EGFP) coupled to a component of an intracellular signalling pathway such as a transcription factor, a cGMP- or cAMP-dependent protein kinase, a cyclin-, calmodulin- or phospholipid-dependent or mitogen-activated serine/threonine protein kinase, a tyrosine protein kinase, or a protein phosphatase (e.g. PKA, PKC, Erk, Smad, VASP, actin, p38, Jnk1, PKG, IkappaB, CDK2, Grk5, Zap70, p85, protein-tyrosine phosphatase 1C, Stat5, NFAT, NFkappaB, RhoA, PKB). An influence modulates the intracellular signalling pathway in such a way that the luminophore is being redistributed or translocated with the component in living cells in a manner experimentally determined to be correlated to the degree of the influence. Measurement of redistribution is performed by recording of light intensity, fluorescence lifetime, polarization, wavelength shift, resonance energy transfer, or other properties by an apparatus consisting of e.g. a fluorescence microscope and a CCD camera. Data stored as digital images are processed to numbers representing the degree of redistribution. The method can be used as a screening program for identifying a compound that modulates a component and is capable of treating a disease related to the function of the component.</p>		

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A METHOD for extracting quantitative information relating to an influence on a cellular response

FIELD OF INVENTION

5 The present invention relates to a method and tools for extracting quantitative information relating to an influence, on a cellular response, in particular an influence caused by contacting or incubating the cell with a substance influencing a cellular response, where the cellular response is manifested in redistribution of at least one component in the cell. In particular, the invention relates to a method for extracting quantitative information relating to an influence
10 ce on an intracellular pathway involving redistribution of at least one component associated with the pathway. The method of the invention may be used as a very efficient procedure for testing or discovering the influence of a substance on a physiological process, for example in connection with screening for new drugs, testing of substances for toxicity, identifying drug targets for known or novel drugs. Other valuable uses of the method and technology of the invention will be apparent to the skilled person on the basis of the following disclosure. In a
15 particular embodiment of the invention, the present invention relates to a method of detecting intracellular translocation or redistribution of biologically active polypeptides, preferably an enzyme, affecting intracellular processes, and a DNA construct and a cell for use in the method.

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BACKGROUND OF THE INVENTION

Intracellular pathways are tightly regulated by a cascade of components that undergo modulation in a temporally and spatially characteristic manner. Several disease states can be attributed to altered activity of individual signalling components (i.e. protein kinases, protein phosphatases, transcription factors). These components therefore render themselves as
25 attractive targets for therapeutic intervention.

Protein kinases and phosphatases are well described components of several intracellular signalling pathways. The catalytic activity of protein kinases and phosphatases are assumed to play a role in virtually all regulatable cellular processes. Although the involvement of protein kinases in cellular signalling and regulation have been subjected to extensive studies,
30 detailed knowledge on e.g. the exact timing and spatial characteristics of signalling events is often difficult to obtain due to lack of a convenient technology.

Novel ways of monitoring specific modulation of intracellular pathways in intact, living cells is assumed to provide new opportunities in drug discovery, functional genomics, toxicology, patient monitoring etc.

5 The spatial orchestration of protein kinase activity is likely to be essential for the high degree of specificity of individual protein kinases. The phosphorylation mediated by protein kinases is balanced by phosphatase activity. Also within the family of phosphatases translocation has been observed, e.g. translocation of PTP2C to membrane ruffles [(Cossette *et al.* 1996)], and likewise is likely to be indicative of phosphatase activity.

10 Protein kinases often show a specific intracellular distribution before, during and after activation. Monitoring the translocation processes and/or redistribution of individual protein kinases or subunits thereof is thus likely to be indicative of their functional activity. A connection between translocation and catalytic activation has been shown for protein kinases like the diacyl glycerol (DAG)-dependent protein kinase C (PKC), the cAMP-dependent protein kinase (PKA) [(DeBernardi *et al.* 1996)] and the mitogen-activated-protein kinase Erk-1 [(Sano *et al.* 1995)].

Commonly used methods of detection of intracellular localisation/activity of protein kinases and phosphatases are immunoprecipitation, Western blotting and immunocytochemical detection.

20 Taking the family of diacyl glycerol (DAG)-dependent protein kinase Cs (PKCs) as an example, it has been shown that individual PKC isoforms that are distributed among different tissues and cells have different activator requirements and undergo differential translocation in response to activation. Catalytically inactive DAG-dependent PKCs are generally distributed throughout the cytoplasm, whereas they upon activation translocate to become associated with different cellular components, e.g. plasma membrane [(Farese, 1992),(Fulop Jr. *et al.* 1995)] nucleus [(Khalil *et al.* 1992)], cytoskeleton [(Blobe *et al.* 1996)]. The translocation phenomenon being indicative of PKC activation has been monitored using different approaches: a) immunocytochemistry where the localisation of individual isoforms can be detected after permeabilisation and fixation of the cells [(Khalil *et al.* 1992)]; and b) tagging all DAG-dependent PKC isoforms with a fluorescently labelled phorbol myristate acetate (PMA) 25 [(Godson *et al.* 1996)]; and c) chemical tagging PKC b1 with the fluorophore Cy3 [(Bastiaens & Jovin 1996)] and d) genetic tagging of PKC α [(Schmidt *et al.* 1997)] and of PKC γ and PKC ϵ [(Sakai *et al.* 1996)]. The first method does not provide dynamic information whereas the latter methods will. Tagging PKC with fluorescently labelled phorbol myristate acetate cannot

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distinguish between different DAG-dependent isoforms of PKC but will label and show movement of all isoforms. Chemical and genetic labelling of specific DAG-dependent PKCs confirmed that they in an isoform specific manner upon activation move to cell periphery or nucleus.

- 5 In an alternative method, protein kinase A activity has been measured in living cells by chemical labelling one of the kinase's subunit (Adams *et al.* 1991). The basis of the methodology is that the regulatory and catalytic subunit of purified protein kinase A is labelled with fluorescein and rhodamine, respectively. At low cAMP levels protein kinase A is assembled in a heterotetrameric form which enables fluorescence resonance energy transfer between
10 the two fluorescent dyes. Activation of protein kinase A leads to dissociation of the complex, thereby eliminating the energy transfer. A disadvantage of this technology is that the labelled protein kinase A has to be microinjected into the cells of interest. This highly invasive technique is cumbersome and not applicable to large scale screening of biologically active substances. A further disadvantage of this technique as compared to the presented invention is
15 that the labelled protein kinase A cannot be inserted into organisms/animals as a transgene.

Recently it was discovered that Green Fluorescent Protein (GFP) expressed in many different cell types, including mammalian cells, became highly fluorescent [(Chalfie *et al.* 1994)]. WO95/07463 describes a cell capable of expressing GFP and a method for detecting a protein of interest in a cell based on introducing into a cell a DNA molecule having DNA sequence encoding the protein of interest linked to DNA sequence encoding a GFP such that
20 the protein produced by the DNA molecule will have the protein of interest fused to the GFP, then culturing the cells in conditions permitting expression of the fused protein and detecting the location of the fluorescence in the cell, thereby localizing the protein of interest in the cell. However, examples of such fused proteins are not provided, and the use of fusion proteins with GFP for detection or quantitation of translocation or redistribution of biologically
25 active polypeptides affecting intracellular processes upon activation, such as proteins involved in signalling pathways, e.g. protein kinases or phosphatases, has not been suggested. WO 95/07463 further describes cells useful for the detection of molecules, such as hormones or heavy metals, in a biological sample, by operatively linking a regulatory element of the gene which is affected by the molecule of interest to a GFP, the presence of the
30 molecules will affect the regulatory element which in turn will affect the expression of the GFP. In this way the gene encoding GFP is used as a reporter gene in a cell which is constructed for monitoring the presence of a specific molecular identity.

Green Fluorescent Protein has been used in an assay for the detection of translocation of the glucocorticoid receptor (GR) [Carey, KL et al., The Journal of Cell Biology, Vol. 133, No. 5, p. 985-996 (1996)]. A GR-S65TGFP fusion has been used to study the mechanisms involved in translocation of the glucocorticoid receptor (GR) in response to the agonist dexamethasone from the cytosol, where it is present in the absence of a ligand, through the nuclear pore to the nucleus where it remains after ligand binding. The use of a GR-GFP fusion enables real-time imaging and quantitation of nuclear/cytoplasmic ratios of the fluorescence signal.

Many currently used screening programmes designed to find compounds that affect protein kinase activity are based on measurements of kinase phosphorylation of artificial or natural substrates, receptor binding and/or reporter gene expression.

DISCLOSURE OF THE INVENTION

The present invention provides an important new dimension in the investigation of cellular systems involving redistribution in that the invention provides quantification of the redistribution responses or events caused by an influence, typically contact with a chemical substance or mixture of chemical substances, but also changes in the physical environment. The quantification makes it possible to set up meaningful relationships, expressed numerically, or as curves or graphs, between the influences (or the degree of influences) on cellular systems and the redistribution response. This is highly advantageous because, as has been found, the quantification can be achieved in both a fast and reproducible manner, and - what is perhaps even more important - the systems which become quantifiable utilizing the method of the invention are systems from which enormous amounts of new information and insight can be derived.

The present screening assays have the distinct advantage over other screening assays, e.g., receptor binding assays, enzymatic assays, and reporter gene assays, in providing a system in which biologically active substances with completely novel modes of action, e.g. inhibition or promotion of redistribution/translocation of a biologically active polypeptide as a way of regulating its action rather than inhibition/activation of enzymatic activity, can be identified in a way that insures very high selectivity to the particular isoform of the biologically active polypeptide and further development of compound selectivity versus other isoforms of

the same biologically active polypeptide or other components of the same signalling pathway.

In its broadest aspect, the invention relates to a method for extracting quantitative information relating to an influence on a cellular response, the method comprising recording variation, caused by the influence on a mechanically intact living cell or mechanically intact living cells, in spatially distributed light emitted from a luminophore, the luminophore being present in the cell or cells and being capable of being redistributed in a manner which is related with the degree of the influence, and/or of being modulated by a component which is capable of being redistributed in a manner which is related to the degree of the influence, the association resulting in a modulation of the luminescence characteristics of the luminophore, detecting and recording the spatially distributed light from the luminophore, and processing the recorded variation in the spatially distributed light to provide quantitative information correlating the spatial distribution or change in the spatial distribution to the degree of the influence. In a preferred embodiment of the invention the luminophore, which is present in the cell or cells, is capable of being redistributed by modulation of an intracellular pathway, in a manner which is related to the redistribution of at least one component of the intracellular pathway. In another preferred embodiment of the invention, the luminophore is a fluorophore.

The cells

In the invention the cell and/or cells are mechanically intact and alive throughout the experiment. In another embodiment of the invention, the cell or cells is/are fixed at a point in time after the application of the influence at which the response has been predetermined to be significant, and the recording is made at an arbitrary later time.

The mechanically intact living cell or cells could be selected from the group consisting of fungal cell or cells, such as a yeast cell or cells; invertebrate cell or cells including insect cell or cells; and vertebrate cell or cells, such as mammalian cell or cells. This cell or these cells is/are incubated at a temperature of 30°C or above, preferably at a temperature of from 32°C to 39°C, more preferably at a temperature of from 35°C to 38°C, and most preferably at a temperature of about 37°C during the time period over which the influence is observed. In one aspect of the invention the mechanically intact living cell is part of a matrix of identical or non-identical cells.

A cell used in the present invention should contain a nucleic acid construct encoding a fusion polypeptide as defined herein and be capable of expressing the sequence encoded by the construct. The cell is a eukaryotic cell selected from the group consisting of fungal cells, such as yeast cells; invertebrate cells including insect cells; vertebrate cells such as mam-
5 malian cells. The preferred cells are mammalian cells.

In another aspect of the invention the cells could be from an organism carrying in at least one of its component cells a nucleic acid sequence encoding a fusion polypeptide as defined herein and be capable of expressing said nucleic acid sequence. The organism is selected from the group consisting of unicellular and multicellular organisms, such as a mammal.

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The luminophore

The luminophore is the component which allows the redistribution to be visualised and/or recorded by emitting light in a spatial distribution related to the degree of influence. In one embodiment of the invention, the luminophore is capable of being redistributed in a manner
15 which is physiologically relevant to the degree of the influence. In another embodiment, the luminophore is capable of associating with a component which is capable of being redistributed in a manner which is physiologically relevant to the degree of the influence. In another embodiment, the luminophore correlation between the redistribution of the luminophore and the degree of the influence could be determined experimentally. In a preferred aspect of the
20 invention, the luminophore is capable of being redistributed in substantially the same manner as the at least one component of an intracellular pathway. In yet another embodiment of the invention, the luminophore is capable of being quenched upon spatial association with a component which is redistributed by modulation of the pathway, the quenching being measured as a change in the intensity of the luminescence.

25 The luminophore could be a fluorophore. In a preferred embodiment of the invention, the luminophore could be a polypeptide encoded by and expressed from a nucleotide sequence harboured in the cell or cells. The luminophore could be a hybrid polypeptide comprising a fusion of at least a portion of each of two polypeptides one of which comprises a luminescent polypeptide and the other one of which comprises a biologically active polypeptide, as defined
30 herein.

The luminescent polypeptide could be a GFP as defined herein or could be selected from the group consisting of green fluorescent proteins having the F64L mutation as defined herein

such as F64L-GFP, F64L-Y66H-GFP, F64L-S65T-GFP, and EGFP. The GFP could be N- or C-terminally tagged, optionally via a peptide linker, to the biologically active polypeptide or a part or a subunit thereof. The fluorescent probe could be a component of an intracellular signalling pathway. The probe is coded for by a nucleic acid construct.

- 5 The pathway of investigation in the present invention could be an intracellular signalling pathway.

The influence

- 10 In a preferred embodiment of the invention, the influence could be contact between the mechanically intact living cell or the group of mechanically intact living cells with a chemical substance and/or incubation of the mechanically intact living cell or the group of mechanically intact living cells with a chemical substance. The influence will modulate the intracellular processes. In one aspect the modulation could be an activation of the intracellular processes. In another aspect the modulation could be an deactivation of the intracellular processes.
- 15 In yet another aspect, the influence could inhibit or promote the redistribution without directly affecting the metabolic activity of the component of the intracellular processes.

In one embodiment the invention is used as a basis for a screening program, where the effect of unknown influences such as a compound library, can be compared to influence of known reference compounds under standardised conditions.

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The recording

- In addition to the intensity, there are several parameters of fluorescence or luminescence which can be modulated by the effect of the influence on the underlying cellular phenomena, and can therefore be used in the invention. Some examples are resonance energy transfer,
- 25 fluorescence lifetime, polarisation, wavelength shift. Each of these methods requires a particular kind of filter in the emission light path to select the component of the light desired and reject other components. The recording of property of light could be in the form of an ordered array of values such as a CCD array or a vacuum tube device such as a vidicon tube.

- In one embodiment of the invention, the spatially distributed light emitted by a luminophore
- 30 could be detected by a change in the resonance energy transfer between the luminophore and another luminescent entity capable of delivering energy to the luminophore, each of

which has been selected or engineered to become part of, bound to or associated with particular components of the intracellular pathway. In this embodiment, either the luminophore or the luminescent entity capable of delivering energy to the luminophore undergoes redistribution in response to an influence. The resonance energy transfer would be measured as a change in the intensity of emission from the luminophore, preferably sensed by a single channel photodetector which responds only to the average intensity of the luminophore in a non-spatially resolved fashion.

In one embodiment of the invention, the recording of the spatially distributed light could be made at a single point in time after the application of the influence. In another embodiment, the recording could be made at two points in time, one point being before, and the other point being after the application of the influence. The result or variation is determined from the change in fluorescence compared to the fluorescence measured prior to the influence or modulation. In another embodiment of the invention, the recording could be performed at a series of points in time, in which the application of the influence occurs at some time after the first time point in the series of recordings, the recording being performed, e.g., with a predetermined time spacing of from 0.1 seconds to 1 hour, preferably from 1 to 60 seconds, more preferably from 1 to 30 seconds, in particular from 1 to 10 seconds, over a time span of from 1 second to 12 hours, such as from 10 seconds to 12 hours, e.g., from 10 seconds to one hour, such as from 60 seconds to 30 minutes or 20 minutes. The result or variation is determined from the change in fluorescence over time. The result or variation could also be determined as a change in the spatial distribution of the fluorescence over time.

Apparatus

The recording of spatially distributed luminescence emitted from the luminophore is performed by an apparatus for measuring the distribution of fluorescence in the cell or cells, and thereby any change in the distribution of fluorescence in the cell or cells, which includes at a minimum the following component parts: (a) a light source, (b) a method for selecting the wavelength(s) of light from the source which will excite the fluorescence of the protein, (c) a device which can rapidly block or pass the excitation light into the rest of the system, (d) a series of optical elements for conveying the excitation light to the specimen, collecting the emitted fluorescence in a spatially resolved fashion, and forming an image from this fluorescence emission, (e) a bench or stand which holds the container of the cells being measured in a predetermined geometry with respect to the series of optical elements, (f) a detector to

record the spatially resolved fluorescence in the form of an image, (g) a computer or electronic system and associated software to acquire and store the recorded images, and to compute the degree of redistribution from the recorded images.

In a preferred embodiment of the invention the apparatus system is automated. In one embodiment the components in d and e mentioned above comprise a fluorescence microscope.
In one embodiment the component in f mentioned above is a CCD camera.

In one embodiment the image is formed and recorded by an optical scanning system.

In one embodiment a liquid addition system is used to add a known or unknown compound to any or all of the cells in the cell holder at a time determined in advance. Preferably, the liquid addition system is under the control of the computer or electronic system. Such an automated system can be used for a screening program due to its ability to generate results from a larger number of test compounds than a human operator could generate using the apparatus in a manual fashion.

15 Quantitation of the influence

The recording of the variation or result with respect to light emitted from the luminophore is performed by recording the spatially distributed light as one or more digital images, and the processing of the recorded variation to reduce it to one or more numbers representative of the degree of redistribution comprises a digital image processing procedure or combination of digital image processing procedures. The quantitative information which is indicative of the degree of the cellular response to the influence or the result of the influence on the intracellular pathway is extracted from the recording or recordings according to a predetermined calibration based on responses or results, recorded in the same manner, to known degrees of a relevant specific influence. This calibration procedure is developed according to principles described below (Developing an Image-based Assay Technique). Specific descriptions of the procedures for particular assays are given in the examples.

While the stepwise procedure necessary to reduce the image or images to the value representative of the is particular to each assay, the individual steps are generally well-known methods of image processing. Some examples of the individual steps are point operations such as subtraction, ratioing, and thresholding, digital filtering methods such as smoothing, sharpening, and edge detection, spatial frequency methods such as Fourier filtering, image cross-correlation and image autocorrelation, object finding and classification (blob analysis),

and colour space manipulations for visualisation. In addition to the algorithmic procedures, heuristic methods such as neural networks may also be used.

Nucleic acid constructs

5 The nucleic acid constructs used in the present invention encode in their nucleic acid sequences fusion polypeptides comprising a biologically active polypeptide that is a component of an intracellular signalling pathway, or a part thereof, and a GFP, preferably an F64L mutant of GFP, N- or C-terminally fused, optionally via a peptide linker, to the biologically active polypeptide or part thereof.

10 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein kinase or a phosphatase.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a transcription factor or a part thereof which changes cellular localisation upon activation.

15 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein, or a part thereof, which is associated with the cytoskeletal network and which changes cellular localisation upon activation.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein kinase or a part thereof which changes cellular localisation upon activation.

20 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a tyrosine protein kinase or a part thereof capable of changing intracellular localisation upon activation.

25 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a phospholipid-dependent serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.

30 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a cAMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation. In a preferred embodiment the biologically active polypeptide encoded by the nucleic acid construct is a PKAc-F64L-S65T-GFP fusion.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a cGMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation.

5 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a calmodulin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a mitogen-activated serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation. In preferred embodiments the biologically active polypeptide encoded by the nucleic acid constructs are an ERK1-F64L-S65T-GFP fusion or an EGFP-ERK1 fusion.

In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a cyclin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

15 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct is a protein phosphatase or a part thereof capable of changing cellular localisation upon activation.

In one preferred embodiment of the invention the nucleic acid constructs may be DNA constructs.

20 In one embodiment the biologically active polypeptide encoded by the nucleic acid construct In one embodiment the gene encoding GFP in the nucleic acid construct is derived from *Aequorea victoria*. In a preferred embodiment the gene encoding GFP in the nucleic acid construct is EGFP or a GFP variant selected from F64L-GFP, F64L-Y66H-GFP and F64L-S65T-GFP.

25 In preferred embodiments of the invention the DNA constructs which can be identified by any of the DNA sequences shown in SEQ ID NO: 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142 or are variants of these sequences capable of encoding the same fusion polypeptide or a fusion polypeptide which is biologically equivalent thereto, e.g. an isoform, or a splice variant or a homologue from another species.

Screening program

The present invention describes a method that may be used to establish a screening program for the identification of biologically active substances that directly or indirectly affects intracellular signalling pathways and because of this property are potentially useful as medicaments. Based on measurements in living cells of the redistribution of spatially resolved luminescence from luminophores which undergo a change in distribution upon activation or deactivation of an intracellular signalling pathway the result of the individual measurement of each substance being screened indicates its potential biological activity.

In one embodiment of the invention the screening program is used for the identification of a biologically toxic substance as defined herein that exerts its toxic effect by interfering with an intracellular signalling pathway. Based on measurements in living cells of the redistribution of spatially resolved luminescence from luminophores which undergo a change in distribution upon activation or deactivation of an intracellular signalling pathway the result of the individual measurement of each substance being screened indicates its potential biologically toxic activity. In one embodiment of a screening program a compound that modulates a component of an intracellular pathway as defined herein, can be found and the therapeutic amount of the compound estimated by a method according to the method of the invention. In a preferred embodiment the present invention leads to the discovery of a new way of treating a condition or disease related to the intracellular function of a biologically active polypeptide comprising administration to a patient suffering from said condition or disease of an effective amount of a compound which has been discovered by any method according to the invention. In another preferred embodiment of the invention a method is established for identification of a new drug target or several new drug targets among the group of biologically active polypeptides which are components of intracellular signalling pathways.

In another embodiment of the invention an individual treatment regimen is established for the selective treatment of a selected patient suffering from an ailment where the available medicaments used for treatment of the ailment are tested on a relevant primary cell or cells obtained from said patient from one or several tissues, using a method comprising transfecting the cell or cells with at least one DNA sequence encoding a fluorescent probe according to the invention, transferring the transfected cell or cells back the said patient, or culturing the cell or cells under conditions permitting the expression of said probes and exposing it to an array of the available medicaments, then comparing changes in fluorescence patterns or redistribution patterns of the fluorescent probes in the intact living cell or cells to

detect the cellular response to the specific medicaments (obtaining a cellular action profile), then selecting one or more medicament or medicaments based on the desired activity and acceptable level of side effects and administering an effective amount of these medicaments to the selected patient.

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Back-tracking of a signal transduction pathway

The present invention describes a method that may be used to establish a screening program for back-tracking signal transduction pathways as defined herein. In one embodiment the screening program is used to establish more precisely at which level one or several
10 compounds affect a specific signal transduction pathway by successively or in parallel testing the influence of the compound or compounds on the redistribution of spatially resolved luminescence from several of the luminophores which undergo a change in distribution upon activation or deactivation of the intracellular signalling pathway under study.

15 Construction and testing of probes

In general, a probe, i.e. a "GeneX"-GFP fusion or a GFP-"GeneX" fusion, is constructed using PCR with "GeneX"-specific primers followed by a cloning step to fuse "GeneX" in frame with GFP. The fusion may contain a short vector derived sequence between "GeneX" and GFP (e.g. part of a multiple cloning site region in the plasmid) resulting in a peptide linker
20 between "GeneX" and GFP in the resulting fusion protein.

Detailed stepwise procedure:

- Identifying the sequence of the gene. This is most readily done by searching a depository of genetic information, e.g. the GenBank Sequence Database, which is widely available and
25 routinely used by molecular biologists. In the specific examples below the GenBank Accession number of the gene in question is provided.

- Design of gene-specific primers. Inspection of the sequence of the gene allows design of gene-specific primers to be used in a PCR reaction. Typically, the top-strand primer encompasses the ATG start codon of the gene and the following ca. 20 nucleotides, while the
30 bottom-strand primer encompasses the stop codon and the ca. 20 preceding nucleotides, if

the gene is to be fused behind GFP, i.e. a GFP-"GeneX" fusion. If the gene is to be fused in front of GFP, i.e. a "GeneX"-GFP fusion, a stop codon must be avoided. Optionally, the full length sequence of GeneX may not be used in the fusion, but merely the part which localizes and redistributes like GeneX in response to a signal.

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In addition to gene-specific sequences, the primers contain at least one recognition sequence for a restriction enzyme, to allow subsequent cloning of the PCR product. The sites are chosen so that they are unique in the PCR product and compatible with sites in the cloning vector. Furthermore, it may be necessary to include an exact number of nucleotides between
10 the restriction enzyme site and the gene-specific sequence in order to establish the correct reading frame of the fusion gene and/or a translation initiation consensus sequence. Lastly, the primers always contain a few nucleotides in front of the restriction enzyme site to allow efficient digestion with the enzyme.

15 -Identifying a source of the gene to be amplified. In order for a PCR reaction to produce a product with gene-specific primers, the gene-sequence must initially be present in the reaction, e.g. in the form of cDNA. Information in GenBank or the scientific literature will usually indicate in which tissue(s) the gene is expressed, and cDNA libraries from a great variety of tissues or cell types from various species are commercially available, e.g. from Clontech
20 (Palo Alto), Stratagene (La Jolla) and Invitrogen (San Diego). Many genes are also available in cloned form from The American Type Tissue Collection (Virginia).

- Optimizing the PCR reaction. Several factors are known to influence the efficiency and specificity of a PCR reaction, including the annealing temperature of the primers, the concentration of ions, notably Mg^{2+} and K^+ , present in the reaction, as well as pH of the reaction.
25 If the result of a PCR reaction is deemed unsatisfactory, it might be because the parameters mentioned above are not optimal. Various annealing temperatures should be tested, e.g. in a PCR machine with a built-in temperature gradient, available from e.g. Stratagene (La Jolla), and/or various buffer compositions should be tried, e.g. the OptiPrime buffer system from
30 Stratagene (La Jolla).

- Cloning the PCR product. The vector into which the amplified gene product will be cloned and fused with GFP will already have been taken into consideration when the primers were designed. When choosing a vector, one should at least consider in which cell types the probe subsequently will be expressed, so that the promoter controlling expression of the probe is compatible with the cells. Most expression vectors also contain one or more selective markers, e.g. conferring resistance to a drug, which is a useful feature when one wants to make stable transfectants. The selective marker should also be compatible with the cells to be used.
- 10 The actual cloning of the PCR product should present no difficulty as it typically will be a one-step cloning of a fragment digested with two different restriction enzymes into a vector digested with the same two enzymes. If the cloning proves to be problematic, it may be because the restriction enzymes did not work well with the PCR fragment. In this case one could add longer extensions to the end of the primers to overcome a possible difficulty of digestion close to a fragment end, or one could introduce an intermediate cloning step not based on restriction enzyme digestion. Several companies offer systems for this approach, e.g. Invitrogen (San Diego) and Clontech (Palo Alto).

- Once the gene has been cloned and, in the process, fused with the GFP gene, the resulting product, usually a plasmid, should be carefully checked to make sure it is as expected. The most exact test would be to obtain the nucleotide sequence of the fusion-gene.

Testing the probe

- Once a DNA construct for a probe has been generated, its functionality and usefulness may be tested by subjecting it to the following tests:

- Transfecting it into cells capable of expressing the probe. The fluorescence of the cell is inspected soon after, typically the next day. At this point, two features of cellular fluorescence are noted: the intensity and the sub-cellular localization.

The intensity should usually be at least as strong as that of unfused GFP in the cells. If it is not, the sequence or quality of the probe-DNA might be faulty, and should be carefully checked.

- 5 The sub-cellular localization is an indication of whether the probe is likely to perform well. If it localizes as expected for the gene in question, e.g. is excluded from the nucleus, it can immediately go on to a functional test. If the probe is not localized soon after the transfection procedure, it may be because of overexpression at this point in time, as the cell typically will have taken of very many copies of the plasmid, and localization will occur in time, e.g. within
- 10 a few weeks, as plasmid copy number and expression level decreases. If localization does not occur after prolonged time, it may be because the fusion to GFP has destroyed a localization function, e.g. masked a protein sequence essential for interaction with its normal cellular anchor-protein. In this case the opposite fusion might work, e.g. if GeneX-GFP does not work, GFP-GeneX might, as two different parts of GeneX will be affected by the proximity to
- 15 GFP. If this does not work, the proximity of GFP at either end might be a problem, and it could be attempted to increase the distance by incorporating a longer linker between GeneX and GFP in the DNA construct.

If there is no prior knowledge of localization, and no localization is observed, it may be because the probe should not be localized at this point, because such is the nature of the protein fused to GFP. It should then be subjected to a functional test.

20

In a functional test, the cells expressing the probe are treated with at least one compound known to perturb, usually by activating, the signalling pathway on which the probe is expected to report by redistributing itself within the cell. If the redistribution is as expected, e.g. if prior knowledge tell that it should translocate from location X to location Y, it has passed the

25 first critical test. In this case it can go on to further characterization and quantification of the response.

If it does not perform as expected, it may be because the cell lacks at least one component of the signalling pathway, e.g. a cell surface receptor, or there is species incompatibility, e.g. if the probe is modelled on sequence information of a human gene product, and the cell is of

30 hamster origin. In both instances one should identify other cell types for the testing process where these potential problems would not apply.

If there is no prior knowledge about the pattern of redistribution, the analysis of the redistribution will have to be done in greater depth to identify what the essential and indicative features are, and when this is clear, it can go on to further characterization and quantification of the response. If no feature of redistribution can be identified, the problem might be as mentioned above, and the probe should be retested under more optimal cellular conditions.

If the probe does not perform under optimal cellular conditions it's back to the drawing board.

Developing an image-based assay technique

The process of developing an image-based redistribution assay begins with either the unplanned experimental observation that a redistribution phenomenon can be visualised, or the design of a probe specifically to follow a redistribution phenomenon already known to occur. In either event, the first and best exploratory technique is for a trained scientist or technician to observe the phenomenon. Even with the rapid advances in computing technology, the human eye-brain combination is still the most powerful pattern recognition system known, and requires no advance knowledge of the system in order to detect potentially interesting and useful patterns in raw data. This is especially if those data are presented in the form of images, which are the natural "data type" for human visual processing. Because human visual processing operates most effectively in a relatively narrow frequency range, i.e., we cannot see either very fast or very slow changes in our visual field, it may be necessary to record the data and play it back with either time dilation or time compression.

Some luminescence phenomena cannot be seen directly by the human eye. Examples include polarization and fluorescence lifetime. However, with suitable filters or detectors, these signals can be recorded as images or sequences of images and displayed to the human in the fashion just described. In this way, patterns can be detected and the same methods can be applied.

Once the redistribution has been determined to be a reproducible phenomenon, one or more data sets are generated for the purpose of developing a procedure for extracting the quantitative information from the data. In parallel, the biological and optical conditions are determined which will give the best quality raw data for the assay. This can become an iterative process; it may be necessary to develop a quantitative procedure in order to assess the effect on the assay of manipulating the assay conditions.

The data sets are examined by a person or persons with knowledge of the biological phenomenon and skill in the application of image processing techniques. The goal of this exercise is to determine or at least propose a method which will reduce the image or sequence of images constituting the record of a "response" to a value corresponding to the degree of the response. Using either interactive image processing software or an image processing toolbox and a programming language, the method is encoded as a procedure or algorithm which takes the image or images as input and generates the degree of response (in any units) as its output. Some of the criteria for evaluating the validity of a particular procedure are:

- Does the degree of the response vary in a biologically significant fashion, i.e., does it show the known or putative dependence on the concentration of the stimulating agent or condition?
- Is the degree of response reproducible, i.e., does the same concentration or level of stimulating agent or condition give the same response with an acceptable variance?
- Is the dynamic range of the response sufficient for the purpose of the assay? If not, can a change in the procedure or one of its parameters improve the dynamic range?
- Does the procedure exhibit any clear "pathologies", i.e., does it give ridiculous values for the response if there are commonly occurring imperfections in the imaging process? Can these pathologies be eliminated, controlled, or accounted for?
- Can the procedure deal with the normal variation in the number and/or size of cells in an image?

In some cases the method may be obvious; in others, a number of possible procedures may suggest themselves. Even if one method appears clearly superior to others, optimisation of parameters may be required. The various procedures are applied to the data set and the criteria suggested above are determined, or the single procedure is applied repeatedly with adjustment of the parameter or parameters until the most satisfactory combination of signal, noise, range, etc. are arrived at. This is equivalent to the calibration of any type of single-channel sensor.

The number of ways of extracting a single value from an image are extremely large, and thus an intelligent approach must be taken to the initial step of reducing this number to a small, finite number of possible procedures. This is not to say that the procedure arrived at is

necessarily the best procedure - but a global search for the best procedure is simply out of the question due to the sheer number of possibilities involved.

Image-based assays are no different than other assay techniques in that their usefulness is characterised by parameters such as the specificity for the desired component of the sample, the dynamic range, the variance, the sensitivity, the concentration range over which the assay will work, and other such parameters. While it is not necessary to characterise each and every one of these before using the assay, they represent the only way to compare one assay with another.

10 Example: Developing a Quantitative assay for GLUT4 Translocation

GLUT4 is a member of the class of glucose transporter molecules which are important in cellular glucose uptake. It is known to translocate to the plasma membrane under some conditions of stimulation of glucose uptake. The ability to visualize the glucose uptake response noninvasively, without actually measuring glucose uptake, would be a very useful assay for anyone looking for, for example, treatments for type II diabetes.

A CHO cell line which stably expressed the human insulin receptor was used as the basis for a new cell line which stably expressed a fusion between GLUT4 and GFP. This cell line was expected to show translocation of GLUT4 to the plasma membrane as visualized by the movement of the GFP. The translocation could definitely be seen in the form of the appearance of local increases in the fluorescence in regions of the plasma membrane which had a characteristic shape or pattern. This is shown in Figure 12.

These objects became known as "snirclles", and the phenomenon of their appearance as "snircling". In order to quantitate their appearance, a method had to be found to isolate them as objects in the image field, and then enumerate them, measure their area, or determine some parameter about them which correlated in a dose-dependent fashion with the concentration of insulin to which the cells had been exposed. In order to separate the snirclles, a binarization procedure was applied in which one copy of the image smoothed with a relatively severe gaussian kernel ($\sigma = 2.5$) was subtracted from another copy to which only a relatively light gaussian smooth had been applied ($\sigma = 0.5$). The resultant image was rescaled to its min/max range, and an automatic threshold was applied to divide the image into two levels. The thresholded image contains a background of one value all found object with another value. The found objects were first filtered through a filter to remove objects far too

large and far too small to be snircles. The remaining objects, which represent snircles and other artifacts from the image with approximately the same size and intensity characteristics as snircles, are passed into a classification procedure which has been previously trained with many images of snircles to recognize snircles and exclude the other artifacts. The result of this procedure is a binary image which shows only the found snircles to the degree to which the classification procedure can accurately identify them. The total area of the snircles is then summed and this value is the quantitative measure of the degree of snircling for that image.

10 **Definitions:**

In the present specification and claims, the term "an influence" covers any influence to which the cellular response comprises a redistribution. Thus, e.g., heating, cooling, high pressure, low pressure, humidifying, or drying are influences on the cellular response on which the resulting redistribution can be quantified, but as mentioned above, perhaps the most important influences are the influences of contacting or incubating the cell or cells with substances which are known or suspected to exert an influence on the cellular response involving a redistribution contribution. In another embodiment of the invention the influence could be substances from a compound drug library.

20 In the present context, the term "green fluorescent protein" is intended to indicate a protein which, when expressed by a cell, emits fluorescence upon exposure to light of the correct excitation wavelength (cf. [(Chalfie et al. 1994)]). In the following, GFP in which one or more amino acids have been substituted, inserted or deleted is most often termed "modified GFP". "GFP" as used herein includes wild-type GFP derived from the jelly fish *Aequorea victoria* and modifications of GFP, such as the blue fluorescent variant of GFP disclosed by Heim et al. (1994). Proc.Natl.Acad.Sci. 91:12501, and other modifications that change the spectral properties of the GFP fluorescence, or modifications that exhibit increased fluorescence when expressed in cells at a temperature above about 30°C described in PCT/DK96/00051, published as WO 97/11094 on 27 March 1997 and hereby incorporated by reference, and which comprises a fluorescent protein derived from *Aequorea* Green Fluorescent Protein (GFP) or any functional analogue thereof, wherein the amino acid in position 1 upstream from the chromophore has been mutated to provide an increase of fluorescence intensity when the

fluorescent protein of the invention is expressed in cells. Preferred GFP variants are F64L-GFP, F64L-Y66H-GFP and F64L-S65T-GFP. An especially preferred variant of GFP for use in all the aspects of this invention is EGFP (DNA encoding EGFP which is a F64L-S65T variant with codons optimized for expression in mammalian cells is available from Clontech, Palo Alto, plasmids containing the EGFP DNA sequence, cf. GenBank Acc. Nos. U55762, U55763).

The term "intracellular signalling pathway" and "signal transduction pathway" are intended to indicate the coordinated intracellular processes whereby a living cell transduce an external or internal signal into cellular responses. Said signal transduction will involve an enzymatic reaction said enzymes include but are not limited to protein kinases, GTPases, ATPases, protein phosphatases, phospholipases. The cellular responses include but are not limited to gene transcription, secretion, proliferation, mechanical activity, metabolic activity, cell death.

The term "second messenger" is used to indicate a low molecular weight component involved in the early events of intracellular signal transduction pathways.

The term "luminophore" is used to indicate a chemical substance which has the property of emitting light either inherently or upon stimulation with chemical or physical means. This includes but is not limited to fluorescence, bioluminescence, phosphorescence, chemiluminescence.

The term "mechanically intact living cell" is used to indicate a cell which is considered living according to standard criteria for that particular type of cell such as maintenance of normal membrane potential, energy metabolism, proliferative capability, and has not experienced any physically invasive treatment designed to introduce external substances into the cell such as microinjection.

The term "physiologically relevant" ,when applied to an experimentally determined redistribution of an intracellular component, as measured by a change in the luminescence properties or distribution, is used to indicate that said redistribution can be explained in terms of the underlying biological phenomenon which gives rise to the redistribution.

Th terms "image processing" and "image analysis" are used to describe a large family of digital data analysis techniques or combination of such techniques which reduce ordered arrays of numbers (images) to quantitative information describing those ordered arrays of numbers. When said ordered arrays of numbers represent measured values from a physical process, the quantitative information derived is therefore a measure of the physical process.

The term "fluorescent probe" is used to indicate a fluorescent fusion polypeptide comprising a GFP or any functional part thereof which is N- or C-terminally fused to a biologically active polypeptide as defined herein, optionally via a peptide linker consisting of one or more amino acid residues, where the size of the linker peptide in itself is not critical as long as the desired functionality of the fluorescent probe is maintained. A fluorescent probe according to the invention is expressed in a cell and basically mimics the physiological behaviour of the biologically active polypeptide moiety of the fusion polypeptide.

The term "mammalian cell" is intended to indicate any living cell of mammalian origin. The cell may be an established cell line, many of which are available from The American Type Culture Collection (ATCC, Virginia, USA) or a primary cell with a limited life span derived from a mammalian tissue, including tissues derived from a transgenic animal, or a newly established immortal cell line derived from a mammalian tissue including transgenic tissues, or a hybrid cell or cell line derived by fusing different celltypes of mammalian origin e.g. hybridoma cell lines. The cells may optionally express one or more non-native gene products, e.g. receptors, enzymes, enzyme substrates, prior to or in addition to the fluorescent probe. Preferred cell lines include but are not limited to those of fibroblast origin, e.g. BHK, CHO, BALB, or of endothelial origin, e.g. HUVEC, BAE (bovine artery endothelial), CPAE (cow pulmonary artery endothelial) or of pancreatic origin, e.g. RIN, INS-1, MIN6, bTC3, aTC6, bTC6, HIT, or of hematopoietic origin, e.g. adipocyte origin, e.g. 3T3-L1, neuronal/neuroendocrine origin, e.g. AtT20, PC12, GH3, muscle origin, e.g. SKMC, A10, C2C12, renal origin, e.g. HEK 293, LLC-PK1.

The term "hybrid polypeptide" is intended to indicate a polypeptide which is a fusion of at least a portion of each of two proteins, in this case at least a portion of the green fluorescent protein, and at least a portion of a catalytic and/or regulatory domain of a protein kinase. Furthermore a hybrid polypeptide is intended to indicate a fusion polypeptide comprising a

GFP or at least a portion of the green fluorescent protein that contains a functional fluorophore, and at least a portion of a biologically active polypeptide as defined herein provided that said fusion is not the PKC α -GFP, PKC γ -GFP, and PKC ϵ -GFP disclosed by Schmidt et al. and Sakai et al., respectively. Thus, GFP may be N- or C-terminally tagged to a biologically active polypeptide, optionally via a linker portion or linker peptide consisting of a sequence of one or more amino acids. The hybrid polypeptide or fusion polypeptide may act as a fluorescent probe in intact living cells carrying a DNA sequence encoding the hybrid polypeptide under conditions permitting expression of said hybrid polypeptide.

- 10 The term "kinase" is intended to indicate an enzyme that is capable of phosphorylating a cellular component.

The term "protein kinase" is intended to indicate an enzyme that is capable of phosphorylating serine and/or threonine and/or tyrosine in peptides and/or proteins.

- 15 The term "phosphatase" is intended to indicate an enzyme that is capable of dephosphorylating phosphoserine and/or phosphothreonine and/or phosphotyrosine in peptides and/or proteins.

- In the present context, the term "biologically active polypeptide" is intended to indicate a polypeptide affecting intracellular processes upon activation, such as an enzyme which is active in intracellular processes or a portion thereof comprising a desired amino acid sequence which has a biological function or exerts a biological effect in a cellular system. In the polypeptide one or several amino acids may have been deleted, inserted or replaced to alter its biological function, e.g. by rendering a catalytic site inactive. Preferably, the biologically active polypeptide is selected from the group consisting of proteins taking part in an intracellular signalling pathway, such as enzymes involved in the intracellular phosphorylation and dephosphorylation processes including kinases, protein kinases and phosphorylases as defined herein, but also proteins making up the cytoskeleton play important roles in intracellular signal transduction and are therefore included in the meaning of "biologically active polypeptide" herein. More preferably, the biologically active polypeptide is a protein which according to its state as activated or non-activated changes localisation within the cell, preferably as an in-

termediary component in a signal transduction pathway. Included in this preferred group of biologically active polypeptides are cAMP dependent protein kinase A.

5 The term "a substance having biological activity" is intended to indicate any sample which has a biological function or exerts a biological effect in a cellular system. The sample may be a sample of a biological material such as a sample of a body fluid including blood, plasma, saliva, milk, urine, or a microbial or plant extract, an environmental sample containing pollutants including heavy metals or toxins, or it may be a sample containing a compound or mixture of compounds prepared by organic synthesis or genetic techniques.

10

The phrase "any change in fluorescence" means any change in absorption properties, such as wavelength and intensity, or any change in spectral properties of the emitted light, such as a change of wavelength, fluorescence lifetime, intensity or polarisation, or any change in the intracellular localisation of the fluorophore. It may thus be localised to a specific cellular component (e.g. organelle, membrane, cytoskeleton, molecular structure) or it may be evenly distributed throughout the cell or parts of the cell.

15

The phrase "back-tracking of a signal transduction pathway" is intended to indicate.

The term "organism" as used herein indicates any unicellular or multicellular organism preferably originating from the animal kingdom including protozoans, but also organisms that are members of the plant kingdoms, such as algae, fungi, bryophytes, and vascular plants are included in this definition.

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The term "nucleic acid" is intended to indicate any type of poly- or oligonucleic acid sequence, such as a DNA sequence, a cDNA sequence, or an RNA sequence.

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The term "biologically equivalent" as it relates to proteins is intended to mean that a first protein is equivalent to a second protein if the cellular functions of the two proteins may substitute for each other, e.g. if the two proteins are closely related isoforms encoded by different genes, if they are splicing variants, or allelic variants derived from the same gene, if they perform identical cellular functions in different cell types, or in different species. The term "biologically equivalent" as it relates to DNA is intended to mean that a first DNA sequ-

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ence encoding a polypeptide is equivalent to a second DNA sequence encoding a polypeptide if the functional proteins encoded by the two genes are biologically equivalent.

The phrase "back-tracking of a signal transduction pathway" is intended to indicate a process for defining more precisely at what level a signal transduction pathway is affected, either by the influence of chemical compounds or a disease state in an organism. Consider a specific signal transduction pathway represented by the bioactive polypeptides A - B - C - D, with signal transduction from A towards D. When investigating all components of this signal transduction pathway compounds or disease states that influence the activity or redistribution of only D can be considered to act on C or downstream of C whereas compounds or disease states that influence the activity or redistribution of C and D, but not of A and B can be considered to act downstream of B.

The term "fixed cells" is used to mean cells treated with a cytological fixative such as glutaraldehyde or formaldehyde, treatments which serve to chemically cross-link and stabilize soluble and insoluble proteins within the structure of the cell. Once in this state, such proteins cannot be lost from the structure of the now-dead cell.

20

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. CHO cells expressing the PKAc-F64L-S65T-GFP hybrid protein have been treated in HAM's F12 medium with 50 mM forskolin at 37°C. The images of the GFP fluorescence in these cells have been taken at different time intervals after treatment, which were: a) 40 seconds b) 60 seconds c) 70 seconds d) 80 seconds. The fluorescence changes from a punctate to a more even distribution within the (non-nuclear) cytoplasm.

25

Figure 2. Time-lapse analysis of forskolin induced PKAc-F64L-S65T-GFP redistribution. CHO cells, expressing the PKAc-F64L-S65T-GFP fusion protein were analysed by time-lapse fluorescence microscopy. Fluorescence micrographs were acquired at regular intervals from 2 min before to 8 min after the addition of agonist. The cells were challenged with 1 mM forskolin immediately after the upper left image was acquired ($t=0$). Frames were collected at the following times: i) 0, ii) 1, iii) 2, iv) 3, v) 4 and vi) 5 minutes. Scale bar 10 μ m.

Figure 3. Time-lapse analyses of PKAc-F64L-S65T-GFP redistribution in response to various agonists. The effects of 1 mM forskolin (A), 50 mM forskolin (B), 1mM dbcAMP (C) and 100 mM IBMX (D) (additions indicated by open arrows) on the localisation of the PKAc-F64L-S65T-GFP fusion protein were analysed by time-lapse fluorescence microscopy of CHO/PKAc-F64L-S65T-GFP cells. The effect of addition of 10 mM forskolin (open arrow), followed shortly by repeated washing with buffer (solid arrow), on the localisation of the PKAc-F64L-S65T-GFP fusion protein was analysed in the same cells (E). In a parallel experiment, the effect of adding 10 mM forskolin and 100 mM IBMX (open arrow) followed by repeated washing with buffer containing 100 mM IBMX (solid arrow) was analysed (F). Removing forskolin caused PKAc-F64L-S65T-GFP fusion protein to return to the cytoplasmic aggregates while this is prevented by the continued presence of IBMX (F). The effect of 100 nM glucagon (Fig 3G, open arrow) on the localisation of the PKAc-F64L-S65T-GFP fusion protein is also shown for BHK/GR, PKAc-F64L-S65T-GFP cells. The effect of 10 mM norepinephrine (H), solid arrow, on the localisation of the PKAc-F64L-S65T-GFP fusion protein was analysed similarly, in transiently transfected CHO, PKAc-F64L-S65T-GFP cells, pretreated with 10 mM forskolin, open arrow, to increase [cAMP]. N.B. in Fig 3H the x-axis counts the image numbers, with 12 seconds between images. The raw data of each experiment consisted of 60 fluorescence micrographs acquired at regular intervals including several images acquired before the addition of buffer or agonist. The charts (A-G) each show a quantification of the response seen through all the 60 images, performed as described in analysis method 2. The change in total area of the highly fluorescent aggregates, relative to the initial area of fluorescent aggregates is plotted as the ordinate in all graphs in Figure 3, versus time for each experiment. Scale bar 10 μ m.

Figure 4. Dose response curve (two experiments) for forskolin-induced redistribution of the PKAc-F64L-S65T-GFP fusion.

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Figure 5. Time from initiation of a response to half maximal ($t_{1/2max}$) and maximal (t_{max}) PKAc-F64L-S65T-GFP redistribution. The data was extracted from curves such as that shown in "Figure 2." All $t_{1/2max}$ and t_{max} values are given as mean \pm SD and are based on a total of 26-30 cells from 2-3 independent experiments for each forskolin concentration. Since the observed

10 redistribution is sustained over time, the t_{max} values were taken as the earliest time point at which complete redistribution is reached. Note that the values do not relate to the degree of redistribution.

15 Figure 6. Parallel dose response analyses of forskolin induced cAMP elevation and PKAc-F64L-S65T-GFP redistribution. The effects of buffer or 5 increasing concentrations of forskolin on the localisation of the PKAc-F64L-S65T-GFP fusion protein in CHO/PKAc-F64L-S65T-GFP cells, grown in a 96 well plate, were analysed as described above. Computing the ratio of the SD's of fluorescence micrographs taken of the same field of cells, prior to and 30 min

20 after the addition of forskolin, gave a reproducible measure of PKAc-F64L-S65T-GFP redistribution. The graph shows the individual 48 measurements and a trace of their mean \pm s.e.m at each forskolin concentration. For comparison, the effects of buffer or 8 increasing concentrations of forskolin on [cAMP]_i was analysed by a scintillation proximity assay of cells grown under the same conditions. The graph shows a trace of the mean \pm s.e.m of 4

25 experiments expressed in arbitrary units.

Figure 7. BHK cells stably transfected with the human muscarinic (hM1) receptor and the PKCa-F64L-S65T-GFP fusion. Carbachol (100 mM added at 1.0 second) induced a transient redistribution of PKCa-F64L-S65T-GFP from the cytoplasm to the plasma membrane. Images were taken at the following times: a) 1 second before carbachol addition, b) 8.8 seconds

30 after addition and c) 52.8 seconds after addition.

Figure 8. BHK cells stably transfected with the hM1 receptor and PKCa-F64L-S65T-GFP fusion were treated with carbachol (1 mM, 10 mM, 100 mM). In single cells intracellular $[Ca^{2+}]$ was monitored simultaneously with the redistribution of PKCa-F64L-S65T-GFP. Dashed line indicates the addition times of carbachol. The top panel shows changes in the intracellular Ca^{2+} concentration of individual cells with time for each treatment. The middle panel shows changes in the average cytoplasmic GFP fluorescence for individual cells against time for each treatment. The bottom panel shows changes in the fluorescence of the periphery of single cells, within regions that specifically include the circumferential edge of a cell as seen in normal projection, the regions which offers best chance to monitor changes in the fluorescence intensity of the plasma membrane.

Figure 9. a) The hERK1-F64L-S65T-GFP fusion expressed in HEK293 cells treated with 100 mM of the MEK1 inhibitor PD98059 in HAM F-12 (without serum) for 30 minutes at 37 °C.

The nuclei empty of fluorescence during this treatment.

b) The same cells as in (a) following treatment with 10 % foetal calf serum for 15 minutes at 37 °C.

c) Time profiles for the redistribution of GFP fluorescence in HEK293 cells following treatment with various concentrations of EGF in Hepes buffer (HAM F-12 replaced with Hepes buffer directly before the experiment). Redistribution of fluorescence is expressed as the change in the ratio value between areas in nucleus and cytoplasm of single cells. Each time profile is the mean for the changes seen in six single cells.

d) Bar chart for the end-point measurements, 600 seconds after start of EGF treatments, of fluorescence change (nucleus:cytoplasm) following various concentrations of EGF.

Figure 10.

a) The SMAD2-EGFP fusion expressed in HEK293 cells starved of serum overnight in HAM F-12. HAM F-12 was then replaced with Hepes buffer pH 7.2 immediately before the experiment. Scale bar is 10 mm.

b) HEK 293 cells expressing the SMAD2-EGFP fusion were treated with various concentration of TGF-beta as indicated, and the redistribution of fluorescence monitored against time.

The time profile plots represent increases in fluorescence within the nucleus, normalised to starting values in each cell measured. Each trace is the time profile for a single cell nucleus.

- c) A bar chart representing the end-point change in fluorescence within nuclei (after 850 seconds of treatment) for different concentrations of TGF-beta. Each bar is the value for a single nucleus in each treatment.

Figure 11. The VASP-F64L-S65T-GFP fusion in CHO cells stably transfected with the human insulin receptor. The cells were starved for two hours in HAM F-12 without serum, then treated with 10% foetal calf serum. The image shows the resulting redistribution of fluorescence after 15 minutes of treatment. GFP fluorescence becomes localised in structures identified as focal adhesions along the length of actin stress fibres.

Figure 12. Time lapse recording GLUT4-GFP redistribution in CHO-HIR cells. Time indicates minutes after the addition of 100 nM insulin.

EXAMPLE 1

- 5 Construction, testing and implementation of an assay for cAMP based on PKA activation in real time within living cells.

Useful for monitoring the activity of signalling pathways which lead to altered concentrations of cAMP, e.g. activation of G-protein coupled receptors which couple to G-proteins of the G_s or G_i class.

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The catalytic subunit of the murine cAMP dependent protein kinase (PKAc) was fused C-terminally to a F64L-S65T derivative of GFP. The resulting fusion (PKAc-F64L-S65T-GFP) was used for monitoring *in vivo* the translocation and thereby the activation of PKA.

Construction of the PKAc-F64L-S65T-GFP fusion:

- 15 Convenient restriction endonuclease sites were introduced into the cDNAs encoding murine PKAc (Gen Bank Accession number: M12303) and F64L-S65T-GFP (sequence disclosed in WO 97/11094) by polymerase chain reaction (PCR). The PCR reactions were performed according to standard protocols with the following primers:

20 5'PKAc: TTggACACAAgCTTTggACACCCTCAggATATgggCAACgCCgCCgCCgCCAAg
(SEQ ID NO:3),

3'PKAc: gTCATCTTCTCgAgTCTTTCAGgCgCgCCCAAACCTCAgTAAACTCCTTgCCACAC
(SEQ ID NO:4) ,

5'GFP: TTggACACAAgCTTTggACACggCgCgCCATgAgTAAAggAgAAgAACTTTTC (SEQ ID NO:1),

- 25 3'GFP: gTCATCTTCTCgAgTCTTACTCCTgAggTTTgTATAgTTCATCCATgCCATgT (SEQ ID NO:2).

The PKAc amplification product was then digested with HindIII+Ascl and the F64L-S65T-GFP product with Ascl+XhoI. The two digested PCR products were subsequently ligated with a HindIII+XhoI digested plasmid (pZeoSV® mammalian expression vector, Invitrogen, San Diego, CA, USA). The resulting fusion construct (SEQ ID NO:68 & 69) was under control of the SV40 promoter.

Transfection and cell culture conditions.

Chinese hamster ovary cells (CHO), were transfected with the plasmid containing the PKAc-F64L-S65T-GFP fusion using the calcium phosphate precipitate method in HEPES-buffered saline (Sambrook *et al.*, 1989). Stable transfectants were selected using 1000 mg Zeocin/ml (Invitrogen) in the growth medium (DMEM with 1000 mg glucose/l, 10 % fetal bovine serum (FBS), 100 mg penicillin-streptomycin mixture ml⁻¹, 2 mM L-glutamine purchased from Life Technologies Inc., Gaithersburg, MD, USA). Untransfected CHO cells were used as the control. To assess the effect of glucagon on fusion protein translocation, the PKAc-F64L-S65T-GFP fusion was stably expressed in baby hamster kidney cells overexpressing the human glucagon receptor (BHK/GR cells) Untransfected BHK/GR cells were used as the control. Expression of GR was maintained with 500 mg G418/ml (Neo marker) and PKAc-F64L-S65T-GFP was maintained with 500 mg Zeocin/ml (*Sh ble* marker). CHO cells were also simultaneously co-transfected with vectors containing the PKAc-F64L-S65T-GFP fusion and the human $\alpha 2a$ adrenoceptor (hAR $\alpha 2a$).

For fluorescence microscopy, cells were allowed to adhere to Lab-Tek chambered cover-glasses (Nalge Nunc Int., Naperville, IL, USA) for at least 24 hours and cultured to about 80% confluence. Prior to experiments, the cells were cultured over night without selection pressure in HAM F-12 medium with glutamax (Life Technologies), 100 mg penicillin-streptomycin mixture ml⁻¹ and 0.3 % FBS. This medium has low autofluorescence enabling fluorescence microscopy of cells straight from the incubator.

Monitoring activity of PKA activity in real time:

Image aquisition of live cells were gathered using a Zeiss Axiovert 135M fluorescence microscope fitted with a Fluar 40X, NA: 1.3 oil immersion objective and coupled to a Photometrics CH250 charged coupled device (CCD) camera. The cells were illuminated with a 100 W HBO arc lamp. In the light path was a 470±20 nm excitation filter, a 510 nm dichroic mirror

and a 515 ± 15 nm emission filter for minimal image background. The cells were kept and monitored to be at 37°C with a custom built stage heater.

Images were processed and analyzed in the following manner:

Method 1: Stepwise procedure for quantitation of translocation of PKA:

- 5 1. The image was corrected for dark current by performing a pixel-by-pixel subtraction of a dark image (an image taken under the same conditions as the actual image, except the camera shutter is not allowed to open).
2. The image was corrected for non-uniformity of the illumination by performing a pixel-by-pixel ratio with a flat field correction image (an image taken under the same conditions as the
- 10 actual image of a uniformly fluorescent specimen).
3. The image histogram, i.e., the frequency of occurrence of each intensity value in the image, was calculated.
4. A smoothed, second derivative of the histogram was calculated and the second zero is determined. This zero corresponds to the inflection point of the histogram on the high side of
- 15 the main peak representing the bulk of the image pixel values.
5. The value determined in step 4 was subtracted from the image. All negative values were discarded.
6. The variance (square of the standard deviation) of the remaining pixel values was determined. This value represents the "response" for that image.
- 20 7. Scintillation proximity assay (SPA) for independent quantitation of cAMP:

Method 2: Alternative method for quantitation of PKA redistribution:

1. The fluorescent aggregates are segmented from each image using an automatically
5 found threshold based on the maximisation of the information measure between the object
and background. The *a priori* entropy of the image histogram is used as the information measure.
2. The area of each image occupied by the aggregates is calculated by counting pixels in
the segmented areas.
- 10 3. The value obtained in step 2 for each image in a series, or treatment pair, is normalised to
the value found for the first (unstimulated) image collected. A value of zero (0) indicates no
redistribution of fluorescence from the starting condition. A value of one (1) by this method
equals full redistribution.

- 15 Cells were cultured in HAM F-12 medium as described above, but in 96-well plates. The medium
was exchanged with Ca^{2+} -HEPES buffer including 100 mM IBMX and the cells were
stimulated with different concentrations of forskolin for 10 min. Reactions were stopped with
addition of NaOH to 0.14 M and the amount of cAMP produced was measured with the
cAMP-SPA kit, RPA538 (Amersham) as described by the manufacturer.

20

Manipulating intracellular levels of cAMP to test the PKAc-F64L-S65T-GFP fusion.

The following compounds were used to vary cAMP levels: Forskolin, an activator of adeny-
late cyclase; dbcAMP, a membrane permeable cAMP analog which is not degraded by
phosphodiesterase; IBMX, an inhibitor of phosphodiesterase.

- 25 CHO cells stably expressing the PKAc-F64L-S65T-GFP, showed a dramatic translocation of
the fusion protein from a punctate distribution to an even distribution throughout the cyto-
plasm following stimulation with 1 mM forskolin (n=3), 10 mM forskolin (n=4) and 50 mM
forskolin (n=4) (Fig 1), or dbcAMP at 1mM (n=6).

Fig. 2 shows the progression of response in time following treatment with 1 mM forskolin.

Fig. 3 gives a comparison of the average temporal profiles of fusion protein redistribution and a measure of the extent of each response to the three forskolin concentrations (Fig. 3A, E, B), and to 1 mM dbcAMP (fig 3C) which caused a similar but slower response, and to addition of 100 mM IBMX (n=4, Fig. 3D) which also caused a slow response, even in the absence of adenylate cyclase stimulation. Addition of buffer (n=2) had no effect (data not shown).

As a control for the behavior of the fusion protein, F64L-S65T-GFP alone was expressed in CHO cells and these were also given 50 mM forskolin (n=5); the uniform diffuse distribution characteristic of GFP in these cells was unaffected by such treatment (data not shown).

10 The forskolin induced translocation of PKAc-F64L-S65T-GFP showed a dose-response relationship (Fig 4 and 6), see quantitative procedures above.

Reversibility of PKAc-F64L-S65T-GFP translocation.

The release of the PKAc probe from its cytoplasmic anchoring hotspots was reversible. 15 Washing the cells repeatedly (5-8 times) with buffer after 10 μ M forskolin treatment completely restored the punctate pattern within 2-5 min (n=2, Fig. 3E). In fact the fusion protein returned to a pattern of fluorescent cytoplasmic aggregates virtually indistinguishable from that observed before forskolin stimulation.

To test whether the return of fusion protein to the cytoplasmic aggregates reflected a decreased [cAMP]_i, cells were treated with a combination of 10 mM forskolin and 100 mM IBMX (n=2) then washed repeatedly (5-8 times) with buffer containing 100 mM IBMX (Fig. 3F). In these experiments, the fusion protein did not return to its prestimulatory localization after removal of forskolin.

25 Testing the PKA-F64L-S65T-GFP probe with physiologically relevant agents.

To test the probe's response to receptor activation of adenylate cyclase, BHK cells stably transfected with the glucagon receptor and the PKA-F64L-S65T-GFP probe were exposed to glucagon stimulation. The glucagon receptor is coupled to a G_s protein which activates adenylate cyclase, thereby increasing the cAMP level. In these cells, addition of 100 nM glucagon (n=2) caused the release of the PKA-F64L-S65T-GFP probe from the cytoplasmic 30 aggregates and a resulting translocation of the fusion protein to a more even cytoplasmic

distribution within 2-3 min (Fig. 3G). Similar but less pronounced effects were seen at lower glucagon concentrations (n=2, data not shown). Addition of buffer (n=2) had no effect over time (data not shown).

Transiently transfected CHO cells expressing hARa2a and the PKA-F64L-S65T-GFP probe were treated with 10 mM forskolin for 7.5 minutes, then, in the continued presence of forskolin, exposed to 10 mM norepinephrine to stimulate the exogenous adrenoreceptors, which couple to a G_i protein, which inhibit adenylate cyclase. This treatment led to reappear-
ance of fluorescence in the cytoplasmic aggregates indicative of a decrease in $[cAMP]_i$ (Fig. 3H).

Fusion protein translocation correlated with $[cAMP]_i$

As described above, the time it took for a response to come to completion was dependent on the forskolin dose (Fig. 5) In addition the degree of responses was also dose dependent. To test the PKA-F64L-S65T-GFP fusion protein translocation in a semi high through-put system, CHO cells stably transfected with the PKA-F64L-S65T-GFP fusion was stimulated with buffer and 5 increasing doses of forskolin (n=8). Using the image analysis algorithm described above (Method 1), a dose response relationship was observed in the range from 0.01-50 mM forskolin (Fig. 6). A half maximal stimulation was observed at about 2 mM forskolin. In parallel, cells were stimulated with buffer and 8 increasing concentrations of forskolin (n=4) in the range 0.01-50 mM. The amount of cAMP produced was measured in an SPA assay. A steep increase was observed between 1 and 5 mM forskolin coincident with the steepest part of the curve for fusion protein translocation (also Fig. 6)

EXAMPLE 2

Quantitation of redistribution in real-time within living cells.

Probe for detection of PKC activity in real time within living cells:

Construction of PKC-GFP fusion:

The probe was constructed by ligating two restriction enzyme treated polymerase chain reaction (PCR) amplification products of the cDNA for murine PKC α (GenBank Accession number: M25811) and F64L-S65T-GFP (sequence disclosed in WO 97/11094) respectively. Taq® polymerase and the following oligonucleotide primers were used for PCR;

5 5'mPKCa: TTggACACAAgCTTTggACACCCTCAggATATggCTgACgTTTACCCggCCAACg
(SEQ ID NO:5),

3'mPKCa: gTCATCTTCTCgAgTCTTTCAggCgCgCCCTACTgCACTTTgCAAgATTgggTgC
(SEQ ID NO:6),

5'F64L-S65T-GFP: TTggACACAAgCTTTggACACggCgCgCCATgAgTAAAggAgAAgAACTT-
10 TTC (SEQ ID NO:1),

3'F64L-S65T-GFP: gTCATCTTCTCgAgTCTTACTCCTgAggTTTgTATAgTTCATCCATgC-
CATgT (SEQ ID NO:2).

The hybrid DNA strand was inserted into the pZeoSV® mammalian expression vector as a HindIII-XhoI cassette as described in example 1.

15 Cell Culture:

BHK cells expressing the human M1 receptor under the control of the inducible metallothionine promoter and maintained with the dihydrofolate reductase marker were transfected with the PKC α -F64L-S65T-GFP probe using the calcium phosphate precipitate method in HEPES buffered saline (HBS [pH 7.10]). Stable transfectants were selected using
20 1000 μ g Zeocin®/ml in the growth medium (DMEM with 1000 mg glucose/l, 10 % foetal bovine serum (FBS), 100 mg penicillin-streptomycin mixture ml⁻¹, 2 mM l-glutamine). The hM1 receptor and PKC α -F64L-S65T-GFP fusion protein were maintained with 500 nM methotrexate and 500 μ g Zeocin®/ml respectively. 24 hours prior to any experiment, the cells were transferred to HAM F-12 medium with glutamax, 100 μ g penicillin-streptomycin
25 mixture ml⁻¹ and 0.3 % FBS. This medium relieves selection pressure, gives a low induction of signal transduction pathways and has a low autofluorescence at the relevant wavelength enabling fluorescence microscopy of cells straight from the incubator.

Monitoring the PKC activity in real time:

Digital images of live cells were gathered using a Zeiss Axiovert 135M fluorescence micro-
30 scope fitted with a 40X, NA: 1.3 oil immersion objective and coupled to a Photometrics

CH250 charged coupled device (CCD) camera. The cells were illuminated with a 100 W arc lamp. In the light path was a 470 ± 20 nm excitation filter, a 510 nm dichroic mirror and a 515 ± 15 nm emission filter for minimal image background. The cells were kept and monitored to be at 37°C with a custom built stage heater.

5 Images were analyzed using the IPLab software package for Macintosh.

Upon stimulation of the M1-BHK cells, stably expressing the PKC α -F64L-S65T-GFP fusion, with carbachol we observed a dose-dependent transient translocation from the cytoplasm to the plasma membrane (Fig. 7a,b,c). Simultaneous measurement of the cytosolic free calcium concentration shows that the carbachol-induced calcium mobilisation precedes the
10 translocation (Fig. 8).

Stepwise procedure for quantitation of translocation of PKC:

1. The image was corrected for dark current by performing a pixel-by-pixel subtraction of a dark image (an image taken under the same conditions as the actual image, except the camera shutter is not allowed to open).
- 15 2. The image was corrected for non-uniformity of the illumination by performing a pixel-by-pixel ratio with a flat field correction image (an image taken under the same conditions as the actual image of a uniformly fluorescent specimen).
3. A copy of the image was made in which the edges are identified. The edges in the image are found by a standard edge-detection procedure – convolving the image with a kernel
20 which removes any large-scale unchanging components (i.e., background) and accentuates any small-scale changes (i.e., sharp edges). This image was then converted to a binary image by thresholding. Objects in the binary image which are too small to represent the edges of cells were discarded. A dilation of the binary image was performed to close any gaps in the image edges. Any edge objects in the image which were in contact with the borders of the image are discarded. This binary image represents the edge mask.
25
4. Another copy of image was made via the procedure in step 3. This copy was further processed to detect objects which enclose “holes” and setting all pixels inside the holes to the binary value of the edge, i.e., one. This image represents the whole cell mask.
5. The original image was masked with the edge mask from step 3 and the sum total of all
30 pixel values is determined.

6. The original image was masked with the whole cell mask from step 4 and the sum total of all pixel values was determined.
7. The value from step 5 was divided by the value from step 6 to give the final result, the fraction of fluorescence intensity in the cells which was localized in the edges.

5

EXAMPLE 3

Probes for detection of mitogen activated protein kinase Erk1 redistribution.

Useful for monitoring signalling pathways involving MAPK, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Erk1, a serine/threonine protein kinase, is a component of a signalling pathway which is activated by e.g. many growth factors.

Probes for detection of ERK-1 activity in real time within living cells:

- 15 The extracellular signal regulated kinase (ERK-1, a mitogen activated protein kinase, MAPK) is fused N- or C-terminally to a derivative of GFP. The resulting fusions expressed in different mammalian cells are used for monitoring *in vivo* the nuclear translocation, and thereby the activation, of ERK1 in response to stimuli that activate the MAPK pathway.

a) Construction of murine ERK1 - F64L-S65T-GFP fusion:

- 20 Convenient restriction endonuclease sites are introduced into the cDNAs encoding murine ERK1 (GenBank Accession number: Z14249) and F64L-S65T-GFP (sequence disclosed in WO 97/11094) by polymerase chain reaction (PCR). The PCR reactions are performed according to standard protocols with the following primers:

5'ERK1: TTggACACAAgCTTTggACACCCTCAggATATggCggCggCggCggCggCTCCggggg-
25 gCgggg (SEQ ID NO:7),

3'ERK1: gTCATCTTCTCgAgTCTTTCAGgCgCgCCCggggCCCTCTggCgCCCCTggCTgg
(SEQ ID NO:8),

5'F64L-S65T-GFP: TTggACACAAgCTTTggACACggCgCgCCATgAgTAAAggAgAAgAACTT-
TTC (SEQ ID NO:1)

- 5 3'F64L-S65T-GFP: gTCATCTTCTCgAgTCTTACTCCTgAggTTTgTATAgTTCATCCATgC-
CATgT (SEQ ID NO:2)

To generate the mERK1-F64L-S65T-GFP (SEQ ID NO:56 & 57) fusion the ERK1 amplifica-
tion product is digested with HindIII+Ascl and the F64L-S65T-GFP product with Ascl+XhoI.
To generate the F64L-S65T-GFP-mERK1 fusion the ERK1 amplification product is then di-
10 gested with HindIII+Bsu36I and the F64L-S65T-GFP product with Bsu36I+XhoI. The two
pairs of digested PCR products are subsequently ligated with a HindIII+XhoI digested plas-
mid (pZeoSV® mammalian expression vector, Invitrogen, San Diego, CA, USA). The resul-
ting fusion constructs are under control of the SV40 promoter.

- 15 b) The human Erk1 gene (GenBank Accession number: X60188) was amplified using PCR
according to standard protocols with primers Erk1-top (SEQ ID NO:9) and Erk1-
bottom/+stop (SEQ ID NO:10) . The PCR product was digested with restriction enzymes E-
coRI and BamHI, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession
number U55763) digested with EcoRI and BamHI. This produces an EGFP-Erk1 fusion
20 (SEQ ID NO:38 &39) under the control of a CMV promoter.

The plasmid containing the EGFP-Erk1 fusion was transfected into HEK293 cells employing
the FUGENE transfection reagent (Boehringer Mannheim). Prior to experiments the cells
were grown to 80%-90% confluency 8 well chambers in DMEM with 10% FCS. The cells we-
25 re washed in plain HAM F-12 medium (without FCS), and then incubated for 30-60 minutes
in plain HAM F-12 (without FCS) with 100 micromolar PD98059, an inhibitor of MEK1, a ki-
nase which activates Erk1; this step effectively empties the nucleus of EGFP-Erk1. Just be-
fore starting the experiment, the HAM F-12 was replaced with Hepes buffer following a wash
with Hepes buffer. This removes the PD98059 inhibitor; if blocking of MEK1 is still wanted
30 (e.g. in control experiments), the inhibitor is included in the Hepes buffer.

The experimental setup of the microscope was as described in example 1.

60 images were collected with 10 seconds between each, and with the test compound added after image number 10.

5 Addition of EGF (1-100 nM) caused within minutes a redistribution of EGFP-Erk1 from the cytoplasm into the nucleus (Fig. 9a,b).

The response was quantitated as described below and a dose-dependent relationship between EGF concentration and nuclear translocation of EGFP-Erk1 was found (Fig. 9c,d). Redistribution of GFP fluorescence is expressed in this example as the change in the ratio value between areas in nuclear versus cytoplasmic compartments of the cell. Each time profile is
10 the average of nuclear to cytoplasmic ratios from six cells in each treatment.

EXAMPLE 4:

Probes for detection of Erk2 redistribution.

Useful for monitoring signalling pathways involving MAPK, e.g. to identify compounds which
15 modulate the activity of the pathway in living cells.

Erk2, a serine/threonine protein kinase, is closely related to Erk1 but not identical; it is a component of a signalling pathway which is activated by e.g. many growth factors.

a) The rat Erk2 gene (GenBank Accession number: M64300) was amplified using PCR according to standard protocols with primers Erk2-top (SEQ ID NO:11) and Erk2-bottom/+stop (SEQ ID NO:13) The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-Erk2 fusion (SEQ ID NO:40 &41) under the control of a CMV promoter.

25 b) The rat Erk2 gene (GenBank Accession number: M64300) was amplified using PCR according to standard protocols with primers (SEQ ID NO:11) Erk2-top and Erk2-bottom/-stop (SEQ ID NO:12). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produces an Erk2-EGFP fusion (SEQ ID NO:58 &59) under
30 the control of a CMV promoter.

The resulting plasmids were transfected into CHO cells and BHK cells. The cells were grown under standard conditions. Prior to experiments, the cells were starved in medium without serum for 48-72 hours. This led to a predominantly cytoplasmic localization of both probes, especially in BHK cells. 10% fetal calf serum was added to the cells and the fluorescence of the cells was recorded as explained in example 3. Addition of serum caused the probes to redistribute into the nucleus within minutes of addition of serum.

EXAMPLE 5:

10 Probes for detection of Smad2 redistribution.

Useful for monitoring signalling pathways activated by some members of the transforming growth factor-beta family, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Smad 2, a signal transducer, is a component of a signalling pathway which is induced by some members of the TGFbeta family of cytokines.

a) The human Smad2 gene (GenBank Accession number: AF027964) was amplified using PCR according to standard protocols with primers Smad2-top (SEQ ID NO:24) and Smad2-bottom/+stop (SEQ ID NO:26) . The PCR product was digested with restriction enzymes EcoR1 and Acc65I, and ligated into pEGFP-C1 (Clontech; Palo Alto; GenBank Accession number U55763) digested with EcoR1 and Acc65I. This produces an EGFP-Smad2 fusion (SEQ ID NO:50&51) under the control of a CMV promoter.

b) The human Smad2 gene (GenBank Accession number: AF027964) was amplified using PCR according to standard protocols with primers Smad2-top (SEQ ID NO:24) and Smad2-bottom/-stop (SEQ ID NO:25) . The PCR product was digested with restriction enzymes EcoR1 and Acc65I, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and Acc65I. This produces a Smad2-EGFP fusion (SEQ ID NO:74 &75) under the control of a CMV promoter.

30 The plasmid containing the EGFP-Smad2 fusion was transfected into HEK293 cells, where it showed a cytoplasmic distribution. Prior to experiments the cells were grown in 8 well Nunc

chambers in DMEM with 10% FCS to 80% confluency and starved overnight in HAM F-12 medium without FCS.

For experiments, the HAM F-12 medium was replaced with Hepes buffer pH 7.2.

The experimental setup of the microscope was as described in example 1.

- 5 90 images were collected with 10 seconds between each, and with the test compound added after image number 5.

After serum starvation of cells, each nucleus contains less GFP fluorescence than the surrounding cytoplasm (Fig. 10a). Addition of TGFbeta caused within minutes a redistribution of EGFP-Smad2 from the cytoplasm into the nucleus (Fig. 10b).

The redistribution of fluorescence within the treated cells was quantified simply as the fractional increase in nuclear fluorescence normalised to the starting value of GFP fluorescence in the nucleus of each unstimulated cell.

15 EXAMPLE 6:

Probe for detection of VASP redistribution.

Useful for monitoring signalling pathways involving rearrangement of cytoskeletal elements, e.g. to identify compounds which modulate the activity of the pathway in living cells.

VASP, a phosphoprotein, is a component of cytoskeletal structures, which redistributes in response to signals which affect focal adhesions.

- a) The human VASP gene (GenBank Accession number: Z46389) was amplified using PCR according to standard protocols with primers VASP-top (SEQ ID NO:94) and VASP-bottom/+stop (SEQ ID NO:95). The PCR product was digested with restriction enzymes Hind3 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Hind3 and BamH1. This produces an EGFP-VASP fusion (SEQ ID NO:124 & 125) under the control of a CMV promoter.

The resulting plasmid was transfected into CHO cells expressing the human insulin receptor using the calcium-phosphate transfection method. Prior to experiments, cells were grown in 8 well Nunc chambers and starved overnight in medium without FCS.

Experiments are performed in a microscope setup as described in example 1.

10% FCS was added to the cells and images were collected. The EGFP-VASP fusion was redistributed from a somewhat even distribution near the periphery into more localized structures, identified as focal adhesion points (Fig. 11).

5

A large number of further GFP fusions have been made or are in the process of being made, as apparent from the following Examples 7-22 which also suggest suitable host cells and substances for activation of the cellular signalling pathways to be monitored and analyzed.

10

EXAMPLE 7:

Probe for detection of actin redistribution.

- 15 Useful for monitoring signalling pathways involving rearrangement or formation of actin filaments, e.g. to identify compounds which modulate the activity of pathways leading to cytoskeletal rearrangements in living cells.

Actin is a component of cytoskeletal structures, which redistributes in response to very many cellular signals.

20

The actin binding domain of the human alpha-actinin gene (GenBank Accession number: X15804) was amplified using PCR according to standard protocols with primers ABD-top (SEQ ID NO:90) and ABD-bottom/-stop (SEQ ID NO:91). The PCR product was digested with restriction enzymes Hind3 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Hind3 and BamH1. This produced an
25 actin-binding-domain-EGFP fusion (SEQ ID NO:128 &129) under the control of a CMV promoter.

- The resulting plasmid was transfected into CHO cells expressing the human insulin receptor. Cells were stimulated with insulin which caused the actin binding domain-EGFP probe to be-
30 come redistributed into morphologically distinct membrane-associated structures.

Example 8:

Probes for detection of p38 redistribution.

- 5 Useful for monitoring signalling pathways responding to various cellular stress situations, e.g. to identify compounds which modulate the activity of the pathway in living cells, or as a counterscreen.

p38, a serine/threonine protein kinase, is a component of a stress-induced signalling pathway which is activated by many types of cellular stress, e.g. TNFalpha, anisomycin, UV and mitomycin C.

10

a) The human p38 gene (GenBank Accession number: L35253) was amplified using PCR according to standard protocols with primers p38-top (SEQ ID NO:14) and p38-bottom/+stop (SEQ ID NO: 16). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produced an EGFP-p38 fusion (SEQ ID NO:46 &47) under the control of a CMV promoter.

15

b) The human p38 gene (GenBank Accession number: L35253) was amplified using PCR according to standard protocols with primers p38-top (SEQ ID NO:13) and p38-bottom/-stop (SEQ ID NO:15) . The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produced a p38-EGFP fusion (SEQ ID NO:64 &65) under the control of a CMV promoter.

20

The resulting plasmids are transfected into a suitable cell line, e.g. HEK293, in which the EGFP-p38 probe and/or the p38-EGFP probe should change its cellular distribution from predominantly cytoplasmic to nuclear within minutes in response to activation of the signalling pathway with e.g. anisomycin.

25

Example 9:

30 Probes for detection of Jnk1 redistribution.

Useful for monitoring signalling pathways responding to various cellular stress situations, e.g. to identify compounds which modulate the activity of the pathway in living cells, or as a counterscreen.

5 Jnk1, a serine/threonine protein kinase, is a component of a stress-induced signalling pathway different from the p38 described above, though it also is activated by many types of cellular stress, e.g. TNFalpha, anisomycin and UV.

10 a) The human Jnk1 gene (GenBank Accession number: L26318) was amplified using PCR according to standard protocols with primers Jnk-top (SEQ ID NO:17) and Jnk-bottom/+stop (SEQ ID NO:19). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produced an EGFP-Jnk1 fusion (SEQ ID NO:44 &45) under the control of a CMV promoter.

15 b) The human Jnk1 gene (GenBank Accession number: L26318) was amplified using PCR according to standard protocols with primers Jnk-top (SEQ ID NO:17) and Jnk-bottom/-stop (SEQ ID NO:18). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produced a Jnk1-EGFP fusion (SEQ ID NO:62 &63) under the control of a CMV promoter.

20 The resulting plasmids are transfected into a suitable cell line, e.g. HEK293, in which the EGFP-Jnk1 probe and/or the Jnk1-EGFP probe should change its cellular distribution from predominantly cytoplasmic to nuclear in response to activation of the signalling pathway with e.g. anisomycin.

25

Example 10:

Probes for detection of PKG redistribution.

Useful for monitoring signalling pathways involving changes in cyclic GMP levels, e.g. to identify compounds which modulate the activity of the pathway in living cells.

30 PGK, a cGMP-dependent serine/threonine protein kinase, mediates the guanylyl-cyclase/cGMP signal.

a) The human PKG gene (GenBank Accession number: Y07512) is amplified using PCR according to standard protocols with primers PKG-top (SEQ ID NO:81) and PKG-bottom/+stop (SEQ ID NO:83). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-PKG fusion (SEQ ID NO:134 &135) under the control of a CMV promoter.

b) The human PKG gene (GenBank Accession number: Y07512) is amplified using PCR according to standard protocols with primers PKG-top (SEQ ID NO:81) and PKG-bottom/-stop (SEQ ID NO: 82). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produces a PKG-EGFP fusion (SEQ ID NO:136 &137) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. A10, in which the EGFP-PKG probe and/or the PKG-EGFP probe should change its cellular distribution from cytoplasmic to one associated with cytoskeletal elements within minutes in response to treatment with agents which raise nitric oxide (NO) levels.

Example 11:

Probes for detection of IkappaB kinase redistribution.

Useful for monitoring signalling pathways leading to NFkappaB activation, e.g. to identify compounds which modulate the activity of the pathway in living cells.

IkappaB kinase, a serine/threonine kinase, is a component of a signalling pathway which is activated by a variety of inducers including cytokines, lymphokines, growth factors and stress.

a) The alpha subunit of the human IkappaB kinase gene (GenBank Accession number: AF009225) is amplified using PCR according to standard protocols with primers IKK-top (SEQ ID NO:96) and IKK-bottom/+stop (SEQ ID NO:98). The PCR product is digested with restriction enzymes EcoR1 and Acc65I, and ligated into pEGFP-C1 (Clontech, Palo Alto;

GenBank Accession number U55763) digested with EcoR1 and Acc65I. This produces an EGFP-IkappaB-kinase fusion (SEQ ID NO:120 &121) under the control of a CMV promoter.

- b) The alpha subunit of the human IkappaB kinase gene (GenBank Accession number: AF009225) is amplified using PCR according to standard protocols with primers IKK-top (SEQ ID NO:96) and IKK-bottom/-stop (SEQ ID NO:97). The PCR product is digested with restriction enzymes EcoR1 and Acc65I, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and Acc65I. This produces an IkappaB-kinase-EGFP fusion (SEQ ID NO:122 &123) under the control of a CMV promoter.

- The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the EGFP-IkappaB-kinase probe and/or the IkappaB-kinase-EGFP probe should achieve a more cytoplasmic distribution within seconds following stimulation with e.g. TNFalpha.

Example 12:

Probes for detection of CDK2 redistribution.

- Useful for monitoring signalling pathways of the cell cycle, e.g. to identify compounds which modulate the activity of the pathway in living cells.

CDK2, a cyclin-dependent serine/threonine kinase, is a component of the signalling system which regulates the cell cycle.

- a) The human CDK2 gene (GenBank Accession number: X61622) is amplified using PCR according to standard protocols with primers CDK2-top (SEQ ID NO:102) and CDK2-bottom/+stop (SEQ ID NO: 104). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-CDK2 fusion (SEQ ID NO:114 &115) under the control of a CMV promoter.

- b) The human CDK2 gene (GenBank Accession number: X61622) is amplified using PCR according to standard protocols with primers CDK2-top (SEQ ID NO:102) and CDK2-bottom/-stop (SEQ ID NO:103). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produces a CDK2-EGFP fusion (SEQ ID NO:112 &113) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. HEK293 in which the EGFP-CDK2 probe and/or the CDK2-EGFP probe should change its cellular distribution from cytoplasmic in contact-inhibited cells, to nuclear location in response to activation with a number of growth factors, e.g. IGF.

5

Example 13:

Probes for detection of Grk5 redistribution.

Useful for monitoring signalling pathways involving desensitization of G-protein coupled receptors, e.g. to identify compounds which modulate the activity of the pathway in living cells.

- 10 Grk5, a G-protein coupled receptor kinase, is a component of signalling pathways involving membrane bound G-protein coupled receptors.

a) The human Grk5 gene (GenBank Accession number: L15388) is amplified using PCR according to standard protocols with primers Grk5-top (SEQ ID NO:27) and Grk5-
15 bottom/+stop (SEQ ID NO:29). The PCR product is digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with EcoR1 and BamH1. This produces an EGFP-Grk5 fusion (SEQ ID NO:42 &43) under the control of a CMV promoter.

b) The human Grk5 gene (GenBank Accession number: L15388) is amplified using PCR according to standard protocols with primers Grk5-top (SEQ ID NO:27) and Grk5-bottom/-stop
20 (SEQ ID NO:28). The PCR product is digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produces a Grk5-EGFP fusion (SEQ ID NO:60 &61) under the control of a CMV promoter.

- 25 The resulting plasmids are transfected into a suitable cell line, e.g. HEK293 expressing a rat dopamine D1A receptor, in which the EGFP-Grk5 probe and/or the Grk5-EGFP probe should change its cellular distribution from predominantly cytoplasmic to peripheral in response to activation of the signalling pathway with e.g. dopamine.

30 Example 14:

Probes for detection of Zap70 redistribution.

Useful for monitoring signalling pathways involving the T cell receptor, e.g. to identify compounds which modulate the activity of the pathway in living cells.

5 Zap70, a tyrosine kinase, is a component of a signalling pathway which is active in e.g. T-cell differentiation.

a) The human Zap70 gene (GenBank Accession number: L05148) is amplified using PCR according to standard protocols with primers Zap70-top (SEQ ID NO:105) and Zap70-bottom/+stop (SEQ ID NO:107). The PCR product is digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-C1 (GenBank Accession number U55763) digested with EcoR1 and BamH1. This produces an EGFP-Zap70 fusion (SEQ ID NO:108 &109) under the control of a CMV promoter.

15 b) The human Zap70 gene (GenBank Accession number: L05148) is amplified using PCR according to standard protocols with primers Zap70-top (SEQ ID NO:105) and Zap70-bottom/-stop (SEQ ID NO:106). The PCR product is digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produces a Zap70-EGFP fusion (SEQ ID NO:110 &111) under the control of a CMV promoter.

20 The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the EGFP-Zap70 probe and/or the Zap70-EGFP probe should change its cellular distribution from cytoplasmic to membrane-associated within seconds in response to activation of the T cell receptor signalling pathway with e.g. antibodies to CD3epsilon.

Example 15:

25 Probes for detection of p85 redistribution.

Useful for monitoring signalling pathways involving PI-3 kinase, e.g. to identify compounds which modulate the activity of the pathway in living cells.

p85alpha is the regulatory subunit of PI3-kinase which is a component of many pathways involving membrane-bound tyrosine kinase receptors and G-protein-coupled receptors.

a) The human p85alpha gene (GenBank Accession number: M61906) was amplified using PCR according to standard protocols with primers p85-top-C (SEQ ID NO:22) and p85-bottom/+stop (SEQ ID NO:23). The PCR product was digested with restriction enzymes Bgl2 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Bgl2 and BamH1. This produced an EGFP-p85alpha fusion (SEQ ID NO:48 &49) under the control of a CMV promoter.

b) The human p85alpha gene (GenBank Accession number: M61906) was amplified using PCR according to standard protocols with primers p85-top-N (SEQ ID NO:20) and p85-bottom/-stop (SEQ ID NO:21). The PCR product was digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produced a p85alpha-EGFP fusion (SEQ ID NO:66 &67) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. CHO expressing the human insulin receptor, in which the EGFP-p85 probe and/or the p85-EGFP probe may change its cellular distribution from cytoplasmic to membrane-associated within minutes in response to activation of the receptor with insulin.

Example 16:

Probes for detection of protein-tyrosine phosphatase redistribution.

Useful for monitoring signalling pathways involving tyrosine kinases, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Protein-tyrosine phosphatase1C, a tyrosine-specific phosphatase, is an inhibitory component in signalling pathways involving e.g. some growth factors.

a) The human protein-tyrosine phosphatase 1C gene (GenBank Accession number: X62055) is amplified using PCR according to standard protocols with primers PTP-top (SEQ ID NO:99) and PTP-bottom/+stop (SEQ ID NO:101). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and EcoR1. This produces an EGFP-PTP fusion (SEQ ID NO:116 &117) under the control of a CMV promoter.

b) The human protein-tyrosine phosphatase 1C gene (GenBank Accession number: X62055) is amplified using PCR according to standard protocols with primers PTP-top (SEQ ID NO:99) and PTP-bottom/-stop (SEQ ID NO:100). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and EcoR1. This produces a PTP-EGFP fusion (SEQ ID NO:118 &119) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. MCF-7 in which the EGFP-PTP probe and/or the PTP-EGFP probe should change its cellular distribution from cytoplasm to the plasma membrane within minutes in response to activation of the growth inhibitory signalling pathway with e.g. somatostatin.

Example 17:

Probes for detection of Smad4 redistribution.

Useful for monitoring signalling pathways involving most members of the transforming growth factor-beta family, e.g. to identify compounds which modulate the activity of the pathway in living cells.

Smad4, a signal transducer, is a common component of signalling pathways induced by various members of the TGFbeta family of cytokines.

a) The human Smad4 gene (GenBank Accession number: U44378) was amplified using PCR according to standard protocols with primers Smad4-top and Smad4-bottom/+stop (SEQ ID NO:35). The PCR product was digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with EcoR1 and BamH1. This produce an EGFP-Smad4 fusion (SEQ ID NO:52 &53) under the control of a CMV promoter.

b) The human Smad4 gene (GenBank Accession number: U44378) was amplified using PCR according to standard protocols with primers Smad4-top (SEQ ID NO:33) and Smad4-bottom/-stop (SEQ ID NO:34). The PCR product was digested with restriction enzymes EcoR1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with EcoR1 and BamH1. This produced a Smad4-EGFP fusion (SEQ ID NO:76 &77) under the control of a CMV promoter.

The resulting plasmids are transfected into a cell line, e.g. HEK293 in which the EGFP-Smad4 probe and/or the Smad4-EGFP probe should change its cellular distribution within minutes from cytoplasmic to nuclear in response to activation of the signalling pathway with e.g. TGFbeta.

5

Example 18:

Probes for detection of Stat5 redistribution.

Useful for monitoring signalling pathways involving the activation of tyrosine kinases of the Jak family, e.g. to identify compounds which modulate the activity of the pathway in living cells.

10

Stat5, signal transducer and activator of transcription, is a component of signalling pathways which are induced by e.g. many cytokines and growth factors.

a) The human Stat5 gene (GenBank Accession number: L41142) was amplified using PCR according to standard protocols with primers Stat5-top (SEQ ID NO:30) and Stat5-bottom/+stop (SEQ ID NO:32). The PCR product was digested with restriction enzymes Bgl2 and Acc65I, and ligated into pEGFP-C1 (Clontech; Palo Alto; GenBank Accession number U55763) digested with Bgl2 and Acc65I. This produced an EGFP-Stat5 fusion (SEQ ID NO:54 &55) under the control of a CMV promoter.

15

b) The human Stat5 gene (GenBank Accession number: L41142) was amplified using PCR according to standard protocols with primers Stat5-top (SEQ ID NO:30) and Stat5-bottom/-stop (SEQ ID NO:331). The PCR product was digested with restriction enzymes Bgl2 and Acc65I, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Bgl2 and Acc65I. This produced a Stat5-EGFP fusion (SEQ ID NO:78 &79) under the control of a CMV promoter.

20

25

The resulting plasmids are transfected into a suitable cell line, e.g. MIN6 in which the EGFP-Stat5 probe and/or the Stat5-EGFP probe should change its cellular distribution from cytoplasmic to nuclear within minutes in response to activation signalling pathway with e.g. prolactin.

30

Example 19:

Probes for detection of NFAT redistribution.

Useful for monitoring signalling pathways involving activation of NFAT, e.g. to identify compounds which modulate the activity of the pathway in living cells.

- 5 NFAT, an activator of transcription, is a component of signalling pathways which is involved in e.g. immune responses.

a) The human NFAT1 gene (GenBank Accession number: U43342) is amplified using PCR according to standard protocols with primers NFAT-top (SEQ ID NO:84) and NFAT-
10 bottom/+stop (SEQ ID NO:86). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and EcoR1. This produces an EGFP-NFAT fusion (SEQ ID NO:130 &131) under the control of a CMV promoter.

b) The human NFAT gene (GenBank Accession number: U43342) is amplified using PCR
15 according to standard protocols with primers NFAT-top (SEQ ID NO:84) and NFAT-bottom/-stop (SEQ ID NO:85). The PCR product is digested with restriction enzymes Xho1 and EcoR1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and EcoR1. This produces an NFAT-EGFP fusion (SEQ ID NO:132 &133) under the control of a CMV promoter.

20 The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the EGFP-NFAT probe and/or the NFAT-EGFP probe should change its cellular distribution from cytoplasmic to nuclear within minutes in response to activation of the signalling pathway with e.g. antibodies to CD3epsilon.

25 Example 20:

Probes for detection of NFkappaB redistribution.

Useful for monitoring signalling pathways leading to activation of NFkappaB, e.g. to identify compounds which modulate the activity of the pathway in living cells.

NFkappaB, an activator of transcription, is a component of signalling pathways which are responsive to a variety of inducers including cytokines, lymphokines, some immunosuppressive agents.

- 5 a) The human NFkappaB p65 subunit gene (GenBank Accession number: M62399) is amplified using PCR according to standard protocols with primers NFkappaB-top (SEQ ID NO:87) and NFkappaB-bottom/+stop (SEQ ID NO:89). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an
- 10 EGFP-NFkappaB fusion (SEQ ID NO:142 & 143) under the control of a CMV promoter.
- b) The human NFkappaB p65 subunit gene (GenBank Accession number: M62399) is amplified using PCR according to standard protocols with primers NFkappaB-top (SEQ ID NO:87) and NFkappaB-bottom/-stop (SEQ ID NO:88). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; Gen-
- 15 Bank Accession number U55762) digested with Xho1 and BamH1. This produces an NFkappaB-EGFP fusion (SEQ ID NO:140 & 141) under the control of a CMV promoter.
- The resulting plasmids are transfected into a suitable cell line, e.g. Jurkat, in which the EGFP-NFkappaB probe and/or the NFkappaB-EGFP probe should change its cellular distribution from cytoplasmic to nuclear in response to activation of the signalling pathway with
- 20 e.g. TNFalpha.

Example 21:

Probe for detection of RhoA redistribution.

- Useful for monitoring signalling pathways involving RhoA, e.g. to identify compounds which
- 25 modulate the activity of the pathway in living cells.

RhoA, a small GTPase, is a component of many signalling pathways, e.g. LPA induced cytoskeletal rearrangements.

- The human RhoA gene (GenBank Accession number: L25080) was amplified using PCR
- 30 according to standard protocols with primers RhoA-top (SEQ ID NO:92) and RhoA-bottom/+stop (SEQ ID NO:93). The PCR product was digested with restriction enzymes

Hind3 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Hind3 and BamH1. This produced an EGFP-RhoA fusion (SEQ ID NO:126 & 127) under the control of a CMV promoter.

- 5 The resulting plasmid is transfected into a suitable cell line, e.g. Swiss3T3, in which the EGFP-RhoA probe should change its cellular distribution from a reasonably homogenous to a peripheral distribution within minutes of activation of the signalling pathway with e.g. LPA.

Example 22:

Probes for detection of PKB redistribution.

- 10 Useful for monitoring signalling pathways involving PKB e.g. to identify compounds which modulate the activity of the pathway in living cells.

PKB, a serine/threonine kinase, is a component in various signalling pathways, many of which are activated by growth factors.

- 15 a) The human PKB gene (GenBank Accession number: M63167) is amplified using PCR according to standard protocols with primers PKB-top (SEQ ID NO:36) and PKB-bottom/+stop (SEQ ID NO:80). The PCR product is digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-C1 (Clontech, Palo Alto; GenBank Accession number U55763) digested with Xho1 and BamH1. This produces an EGFP-PKB fusion (SEQ ID NO:138 & 139) under the control of a CMV promoter.

- 20 b) The human PKB gene (GenBank Accession number: M63167) was amplified using PCR according to standard protocols with primers PKB-top (SEQ ID NO:36) and PKB-bottom/-stop (SEQ ID NO:37). The PCR product was digested with restriction enzymes Xho1 and BamH1, and ligated into pEGFP-N1 (Clontech, Palo Alto; GenBank Accession number U55762) digested with Xho1 and BamH1. This produced a PKB-EGFP fusion (SEQ ID
25 NO:70 & 71) under the control of a CMV promoter.

The resulting plasmids are transfected into a suitable cell line, e.g. CHO expressing the human insulin receptor, in which the EGFP-PKB probe and/or the PKB-EGFP probe cycles between cytoplasmic and membrane locations during the activation-deactivation process following addition of insulin. The transition should be apparent within minutes.

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SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) APPLICANT: NovoNordisk, BioImage

10 (ii) TITLE OF THE INVENTION: A Method of Detecting Cellular
Translocation of Biologically Active Polypeptides Using
Fluorescence Imaging

(iii) NUMBER OF SEQUENCES: 143

15 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NovoNordisk, BioImage

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(C) CITY: Søborg

(D) STATE: DK

20 (E) COUNTRY: DENMARK

(F) ZIP: 2860

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

25 (B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

30 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: , PV&P R

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER:

35

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGACACAA GCTTTGGACA CGGCGCGCCA TGAGTAAAGG AGAAGAACTT TTC

53

50

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTCATCTTCT CGAGTCTTAC TCCTGAGGTT TGTATAGTTC ATCCATGCCA TGT 53

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGGCAACG CCGCCGCCGC CAAG 54

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 GTCATCTTCT CGAGTCTTTC AGGCGCGCCC AAATCAGTA AACTCCTTGC CACAC 55

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGCTGACG TTTACCCGGC CAACG 55

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC TACTGCACTT TGCAAGATTG GGTGC 55

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGCGGCGG CGGCGGCGGC TCCGGGGGGC 60
GGGG 64

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC GGGGCCCTCT GGCGCCCCTG GCTGG 55

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGAATTCAA CCATGGCGGC GCGGCGGCG 30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAGGATCCCT AGGGGGCCTC CAGCACTCC 29

(2) INFORMATION FOR SEQ ID NO:11:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 TACTCGAGTA ACCATGGCGG CGGCGGCGGC G

31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAGGATCCAT AGATCTGTAT CCTGG

25

(2) INFORMATION FOR SEQ ID NO:13:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

35

TAGGATCCTT AAGATCTGTA TCCTGG

26

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCTCGAGGG AAAATGTCTC AGGAGAGG

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

60

61

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5

ATGGATCCTC GGACTCCATC TCTTCTTG

28

(2) INFORMATION FOR SEQ ID NO:16:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGATCCTC AGGACTCCAT CTCTTCTTG

29

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCTCGAGCC ATCATGAGCA GAAGCAAG

28

35

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45

GTGGATCCCA CTGCTGCACC TGTGCTA

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

61

GTGGATCCTC ACTGCTGCAC CTGTGCTA

28

(2) INFORMATION FOR SEQ ID NO:20:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15

CGCGAATTCC GCCACCATGA GTGCTGAGGG GTACCAGTAC

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGGATCCT GTCGCCTCTG CTGTGCATAT AC

32

30

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: p85-top-C

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGAGATCTA TGAGTGCTGA GGGGTACCAG

30

45

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

55

GGGCGGATCC TCATCGCCTC TGCTGTGCAT ATAC

34

62

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGAATTCGA CCATGTCGTC CATCTTGCCA TTC

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGGTACCCA TGACATGCTT GAGCAACGCA C

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTGGTACCTT ATGACATGCT TGAGCAACGC AC

32

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGAATTCGT CAATGGAGCT GGAAAACATC G

31

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

63

64

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGGATCCCT GCTGCTTCCG GTGGAGTTCG

30

10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGATCCCT AGCTGCTTCC GGTGGAGTTC G

31

25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTAGATCTAC CATGGCGGGC TGGATCCAGG CC

32

35

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTGGTACCCA TGAGAGGGAG CCTCTGGCAG A

31

50

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 GTGGTACCTC ATGAGAGGGA GCCTCTGGCA G 31

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGAATTCAA CCATGGACAA TATGTCTATT ACG 33

20 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

30 GTGGATCCCA GTCTAAAGGT TGTGGGTCTG C 31

(2) INFORMATION FOR SEQ ID NO:35:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

45 GTGGATCCTC AGTCTAAAGG TTGTGGGTCT GC 32

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

66

GTCTCGAGGC ACCATGAGCG ACGTGGC

27

(2) INFORMATION FOR SEQ ID NO:37:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGATCCGA GGCCGTGCTG CTGGCCG

27

15

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1896 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1891
 (D) OTHER INFORMATION:

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

35	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	48
	1 5 10 15	
	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
	20 25 30	
40	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
	35 40 45	
45	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
	50 55 60	
50	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	240
	65 70 75 80	
55	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
	85 90 95	

66

67

	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
20	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
25	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
30	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
35	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
40	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
45	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCA ACC ATG GCG GCG GCG	768
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala	
	245 250 255	
50	GCG GCT CAG GGG GGC GGG GGC GGG GAG CCC CGT AGA ACC GAG GGG GTC	816
	Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val	
	260 265 270	
55	GGC CCG GGG GTC CCG GGG GAG GTG GAG ATG GTG AAG GGG CAG CCG TTC	864
	Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe	
	275 280 285	
60	GAC GTG GGC CCG CGC TAC ACG CAG TTG CAG TAC ATC GGC GAG GGC GCG	912
	Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala	
	290 295 300	
65	TAC GGC ATG GTC AGC TCG GCC TAT GAC CAC GTG CGC AAG ACT CGC GTG	960
	Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val	
	305 310 315 320	

67

68

	GCC ATC AAG AAG ATC AGC CCC TTC GAA CAT CAG ACC TAC TGC CAG CGC	1008
	Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg	
	325 330 335	
5	ACG CTC CGG GAG ATC CAG ATC CTG CTG CGC TTC CGC CAT GAG AAT GTC	1056
	Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu Asn Val	
	340 345 350	
10	ATC GGC ATC CGA GAC ATT CTG CGG GCG TCC ACC CTG GAA GCC ATG AGA	1104
	Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg	
	355 360 365	
15	GAT GTC TAC ATT GTG CAG GAC CTG ATG GAG ACT GAC CTG TAC AAG TTG	1152
	Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu	
	370 375 380	
20	CTG AAA AGC CAG CAG CTG AGC AAT GAC CAT ATC TGC TAC TTC CTC TAC	1200
	Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr	
	385 390 395 400	
	CAG ATC CTG CGG GGC CTC AAG TAC ATC CAC TCC GCC AAC GTG CTC CAC	1248
	Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His	
	405 410 415	
25	CGA GAT CTA AAG CCC TCC AAC CTG CTC AGC AAC ACC ACC TGC GAC CTT	1296
	Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu	
	420 425 430	
30	AAG ATT TGT GAT TTC GGC CTG GCC CGG ATT GCC GAT CCT GAG CAT GAC	1344
	Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp	
	435 440 445	
35	CAC ACC GGC TTC CTG ACG GAG TAT GTG GCT ACG CGC TGG TAC CGG GCC	1392
	His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala	
	450 455 460	
40	CCA GAG ATC ATG CTG AAC TCC AAG GGC TAT ACC AAG TCC ATC GAC ATC	1440
	Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile	
	465 470 475 480	
	TGG TCT GTG GGC TGC ATT CTG GCT GAG ATG CTC TCT AAC CGG CCC ATC	1488
	Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile	
	485 490 495	
45	TTC CCT GGC AAG CAC TAC CTG GAT CAG CTC AAC CAC ATT CTG GGC ATC	1536
	Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile	
	500 505 510	
50	CTG GGC TCC CCA TCC CAG GAG GAC CTG AAT TGT ATC ATC AAC ATG AAG	1584
	Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys	
	515 520 525	
55	GCC CGA AAC TAC CTA CAG TCT CTG CCC TCC AAG ACC AAG GTG GCT TGG	1632
	Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp	
	530 535 540	

69

	GCC AAG CTT TTC CCC AAG TCA GAC TCC AAA GCC CTT GAC CTG CTG GAC	1680
	Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp	
	545 550 555 560	
5	CGG ATG TTA ACC TTT AAC CCC AAT AAA CGG ATC ACA GTG GAG GAA GCG	1728
	Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala	
	565 570 575	
10	CTG GCT CAC CCC TAC CTG GAG CAG TAC TAT GAC CCG ACG GAT GAG CCA	1776
	Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro	
	580 585 590	
15	GTG GCC GAG GAG CCC TTC ACC TTC GCC ATG GAG CTG GAT GAC CTA CCT	1824
	Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro	
	595 600 605	
20	AAG GAG CGG CTG AAG GAG CTC ATC TTC CAG GAG ACA GCA CGC TTC CAG	1872
	Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln	
	610 615 620	
25	CCC GGA GTG CTG GAG GCC C CCTAG	1896
	Pro Gly Val Leu Glu Ala Pro	
	625 630	
30	(2) INFORMATION FOR SEQ ID NO:39:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 631 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: protein	
	(v) FRAGMENT TYPE: internal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
40	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

70

	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	145					150					155					160
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
					165					170					175	
5	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
				180					185					190		
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
				195				200					205			
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
10		210					215					220				
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
	225					230					235					240
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Ala	Ala	Ala
					245					250					255	
15	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Gly	Glu	Pro	Arg	Arg	Thr	Glu	Gly	Val
				260					265					270		
	Gly	Pro	Gly	Val	Pro	Gly	Glu	Val	Glu	Met	Val	Lys	Gly	Gln	Pro	Phe
				275				280					285			
	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Gln	Leu	Gln	Tyr	Ile	Gly	Glu	Gly	Ala
20		290					295					300				
	Tyr	Gly	Met	Val	Ser	Ser	Ala	Tyr	Asp	His	Val	Arg	Lys	Thr	Arg	Val
	305					310					315					320
	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln	Thr	Tyr	Cys	Gln	Arg
					325					330					335	
25	Thr	Leu	Arg	Glu	Ile	Gln	Ile	Leu	Leu	Arg	Phe	Arg	His	Glu	Asn	Val
				340					345					350		
	Ile	Gly	Ile	Arg	Asp	Ile	Leu	Arg	Ala	Ser	Thr	Leu	Glu	Ala	Met	Arg
				355				360					365			
	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu	Tyr	Lys	Leu
30		370					375					380				
	Leu	Lys	Ser	Gln	Gln	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr	Phe	Leu	Tyr
	385					390					395					400
	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn	Val	Leu	His
					405					410					415	
35	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Ser	Asn	Thr	Thr	Cys	Asp	Leu
				420					425					430		
	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ala	Asp	Pro	Glu	His	Asp
				435				440					445			
	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala
40		450					455					460				
	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	Asp	Ile
	465					470					475					480
	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	Pro	Ile
					485					490					495	
45	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	Gly	Ile
				500					505					510		
	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	Met	Lys
				515				520					525			
	Ala	Arg	Asn	Tyr	Leu	Gln	Ser	Leu	Pro	Ser	Lys	Thr	Lys	Val	Ala	Trp
50		530					535					540				
	Ala	Lys	Leu	Phe	Pro	Lys	Ser	Asp	Ser	Lys	Ala	Leu	Asp	Leu	Leu	Asp
	545					550					555					560
	Arg	Met	Leu	Thr	Phe	Asn	Pro	Asn	Lys	Arg	Ile	Thr	Val	Glu	Glu	Ala
					565					570					575	
55	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Thr	Asp	Glu	Pro
				580					585					590		

70

71

Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro
 595 600 605
 Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln
 610 615 620
 5 Pro Gly Val Leu Glu Ala Pro
 625 630

(2) INFORMATION FOR SEQ ID NO:40:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1815
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

25	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
30	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
35	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
40	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
45	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
50	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
55	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
60	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	

71

72

	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130						135					140					
5	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
10	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165					170					175		
15	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
20	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
25	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
30	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
35	GGA	CTC	AGA	TCT	CGA	GTA	ACC	ATG	GCG	GCG	GCG	GCG	GCG	GCG	GGC	CCG	768
	Gly	Leu	Arg	Ser	Arg	Val	Thr	Met	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Pro	
					245					250					255		
40	GAG	ATG	GTC	CGC	GGG	CAG	GTG	TTC	GAC	GTG	GGG	CCG	CGC	TAC	ACT	AAT	816
	Glu	Met	Val	Arg	Gly	Gln	Val	Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Asn	
			260						265					270			
45	CTC	TCG	TAC	ATC	GGA	GAA	GGC	GCC	TAC	GGC	ATG	GTT	TGT	TCT	GCT	TAT	864
	Leu	Ser	Tyr	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr	
			275					280					285				
50	GAT	AAT	CTC	AAC	AAA	GTT	CGA	GTT	GCT	ATC	AAG	AAA	ATC	AGT	CCT	TTT	912
	Asp	Asn	Leu	Asn	Lys	Val	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	
		290					295					300					
55	GAG	CAC	CAG	ACC	TAC	TGT	CAG	AGA	ACC	CTG	AGA	GAG	ATA	AAA	ATC	CTA	960
	Glu	His	Gln	Thr	Tyr	Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu	
	305					310					315					320	
60	CTG	CGC	TTC	AGA	CAT	GAG	AAC	ATC	ATC	GGC	ATC	AAT	GAC	ATC	ATC	CGG	1008
	Leu	Arg	Phe	Arg	His	Glu	Asn	Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg	
					325					330					335		
65	GCA	CCA	ACC	ATT	GAG	CAG	ATG	AAA	GAT	GTA	TAT	ATA	GTA	CAG	GAC	CTC	1056
	Ala	Pro	Thr	Ile	Glu	Gln	Met	Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	
			340						345					350			

73

	ATG GAG ACA GAT CTT TAC AAG CTC TTG AAG ACA CAG CAC CTC AGC AAT	1104
	Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn	
	355 360 365	
5	GAT CAT ATC TGC TAT TTT CTT TAT CAG ATC CTG AGA GGA TTA AAG TAT	1152
	Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr	
	370 375 380	
10	ATA CAT TCA GCT AAT GTT CTG CAC CGT GAC CTC AAG CCT TCC AAC CTC	1200
	Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu	
	385 390 395 400	
15	CTG CTG AAC ACC ACT TGT GAT CTC AAG ATC TGT GAC TTT GGC CTT GCC	1248
	Leu Leu Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala	
	405 410 415	
20	CGT GTT GCA GAT CCA GAC CAT GAT CAT ACA GGG TTC TTG ACA GAG TAT	1296
	Arg Val Ala Asp Pro Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr	
	420 425 430	
25	GTA GCC ACG CGT TGG TAC AGA GCT CCA GAA ATT ATG TTG AAT TCC AAG	1344
	Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys	
	435 440 445	
30	GGT TAT ACC AAG TCC ATT GAT ATT TGG TCT GTG GGC TGC ATC CTG GCA	1392
	Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala	
	450 455 460	
35	GAG ATG CTA TCC AAC AGG CCT ATC TTC CCA GGA AAG CAT TAC CTT GAC	1440
	Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp	
	465 470 475 480	
40	CAG CTG AAT CAC ATC CTG GGT ATT CTT GGA TCT CCA TCA CAG GAA GAT	1488
	Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp	
	485 490 495	
45	CTG AAT TGT ATA ATA AAT TTA AAA GCT AGA AAC TAT TTG CTT TCT CTC	1536
	Leu Asn Cys Ile Ile Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu	
	500 505 510	
50	CCG CAC AAA AAT AAG GTG CCG TGG AAC AGG TTG TTC CCA AAC GCT GAC	1584
	Pro His Lys Asn Lys Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp	
	515 520 525	
55	TCC AAA GCT CTG GAT TTA CTG GAT AAA ATG TTG ACA TTT AAC CCT CAC	1632
	Ser Lys Ala Leu Asp Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His	
	530 535 540	
60	AAG AGG ATT GAA GTT GAA CAG GCT CTG GCC CAC CCG TAC CTG GAG CAG	1680
	Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln	
	545 550 555 560	
65	TAT TAT GAC CCA AGT GAT GAG CCC ATT GCT GAA GCA CCA TTC AAG TTT	1728
	Tyr Tyr Asp Pro Ser Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe	
	565 570 575	

74

GAC ATG GAG CTG GAC GAC TTA CCT AAG GAG AAG CTC AAA GAA CTC ATT 1776
 Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile
 580 585 590

5 TTT GAA GAG ACT GCT CGA TTC CAG CCA GGA TAC AGA TCT TAA 1818
 Phe Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser
 595 600 605

10 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 25 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 30 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 35 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 40 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 45 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 50 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Val Thr Met Ala Ala Ala Ala Ala Gly Pro
 245 250 255
 55 Glu Met Val Arg Gly Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn
 260 265 270

74

75

	Leu	Ser	Tyr	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr
		275						280					285			
	Asp	Asn	Leu	Asn	Lys	Val	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe
		290					295					300				
5	Glu	His	Gln	Thr	Tyr	Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu
		305				310					315					320
	Leu	Arg	Phe	Arg	His	Glu	Asn	Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg
					325					330					335	
	Ala	Pro	Thr	Ile	Glu	Gln	Met	Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu
10					340				345					350		
	Met	Glu	Thr	Asp	Leu	Tyr	Lys	Leu	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn
			355					360					365			
	Asp	His	Ile	Cys	Tyr	Phe	Leu	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr
		370					375					380				
15	Ile	His	Ser	Ala	Asn	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu
					390						395					400
	Leu	Leu	Asn	Thr	Thr	Cys	Asp	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala
					405					410					415	
	Arg	Val	Ala	Asp	Pro	Asp	His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr
20					420				425					430		
	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys
			435					440					445			
	Gly	Tyr	Thr	Lys	Ser	Ile	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala
		450				455						460				
25	Glu	Met	Leu	Ser	Asn	Arg	Pro	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp
		465				470					475					480
	Gln	Leu	Asn	His	Ile	Leu	Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp
					485					490					495	
	Leu	Asn	Cys	Ile	Ile	Asn	Leu	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu
30					500				505					510		
	Pro	His	Lys	Asn	Lys	Val	Pro	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp
			515					520					525			
	Ser	Lys	Ala	Leu	Asp	Leu	Leu	Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His
		530					535					540				
35	Lys	Arg	Ile	Glu	Val	Glu	Gln	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln
		545				550					555					560
	Tyr	Tyr	Asp	Pro	Ser	Asp	Glu	Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe
					565					570					575	
	Asp	Met	Glu	Leu	Asp	Asp	Leu	Pro	Lys	Glu	Lys	Leu	Lys	Glu	Leu	Ile
40					580				585					590		
	Phe	Glu	Glu	Thr	Ala	Arg	Phe	Gln	Pro	Gly	Tyr	Arg	Ser			
			595				600						605			

(2) INFORMATION FOR SEQ ID NO:42:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

55

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2526

75

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

5	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
10	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
15	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
20	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
30	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
35	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
60	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
65	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	

77

	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
5	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
10	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG TCA ATG GAG CTG GAA	768
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu	
	245 250 255	
15	AAC ATC GTG GCC AAC ACG GTC TTG CTG AAA GCC AGG GAA GGG GGC GGA	816
	Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly Gly	
	260 265 270	
20	GGA AAG CGC AAA GGG AAA AGC AAG AAG TGG AAA GAA ATC CTG AAG TTC	864
	Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe	
	275 280 285	
	CCT CAC ATT AGC CAG TGT GAA GAC CTC CGA AGG ACC ATA GAC AGA GAT	912
	Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr Ile Asp Arg Asp	
	290 295 300	
25	TAC TGC AGT TTA TGT GAC AAG CAG CCA ATC GGG AGG CTG CTT TTC CGG	960
	Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg Leu Leu Phe Arg	
	305 310 315 320	
30	CAG TTT TGT GAA ACC AGG CCT GGG CTG GAG TGT TAC ATT CAG TTC CTG	1008
	Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr Ile Gln Phe Leu	
	325 330 335	
35	GAC TCC GTG GCA GAA TAT GAA GTT ACT CCA GAT GAA AAA CTG GGA GAG	1056
	Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu Lys Leu Gly Glu	
	340 345 350	
40	AAA GGG AAG GAA ATT ATG ACC AAG TAC CTC ACC CCA AAG TCC CCT GTT	1104
	Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro Lys Ser Pro Val	
	355 360 365	
	TTC ATA GCC CAA GTT GGC CAA GAC CTG GTC TCC CAG ACG GAG GAG AAG	1152
	Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln Thr Glu Glu Lys	
	370 375 380	
45	CTC CTA CAG AAG CCG TGC AAA GAA CTC TTT TCT GCC TGT GCA CAG TCT	1200
	Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala Cys Ala Gln Ser	
	385 390 395 400	
50	GTC CAC GAG TAC CTG AGG GGA GAA CCA TTC CAC GAA TAT CTG GAC AGC	1248
	Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu Tyr Leu Asp Ser	
	405 410 415	
55	ATG TTT TTT GAC CGC TTT CTC CAG TGG AAG TGG TTG GAA AGG CAA CCG	1296
	Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu Glu Arg Gln Pro	
	420 425 430	

77

78

	GTG ACC AAA AAC ACT TTC AGG CAG TAT CGA GTG CTA GGA AAA GGG GGC	1344
	Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu Gly Lys Gly Gly	
	435 440 445	
5	TTC GGG GAG GTC TGT GCC TGC CAG GTT CGG GCC ACG GGT AAA ATG TAT	1392
	Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr Gly Lys Met Tyr	
	450 455 460	
10	GCC TGC AAG CGC TTG GAG AAG AAG AGG ATC AAA AAG AGG AAA GGG GAG	1440
	Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys Arg Lys Gly Glu	
	465 470 475 480	
15	TCC ATG GCC CTC AAT GAG AAG CAG ATC CTC GAG AAG GTC AAC AGT CAG	1488
	Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys Val Asn Ser Gln	
	485 490 495	
20	TTT GTG GTC AAC CTG GCC TAT GCC TAC GAG ACC AAG GAT GCA CTG TGC	1536
	Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys Asp Ala Leu Cys	
	500 505 510	
25	TTG GTC CTG ACC ATC ATG AAT GGG GGT GAC CTG AAG TTC CAC ATC TAC	1584
	Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys Phe His Ile Tyr	
	515 520 525	
30	AAC ATG GGC AAC CCT GGC TTC GAG GAG GAG CGG GCC TTG TTT TAT GCG	1632
	Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala Leu Phe Tyr Ala	
	530 535 540	
35	GCA GAG ATC CTC TGC GGC TTA GAA GAC CTC CAC CGT GAG AAC ACC GTC	1680
	Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg Glu Asn Thr Val	
	545 550 555 560	
40	TAC CGA GAT CTG AAA CCT GAA AAC ATC CTG TTA GAT GAT TAT GGC CAC	1728
	Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Asp Tyr Gly His	
	565 570 575	
45	ATT AGG ATC TCA GAC CTG GGC TTG GCT GTG AAG ATC CCC GAG GGA GAC	1776
	Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile Pro Glu Gly Asp	
	580 585 590	
50	CTG ATC CGC GGC CGG GTG GGC ACT GTT GGC TAC ATG GCC CCC GAA GTC	1824
	Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met Ala Pro Glu Val	
	595 600 605	
55	CTG AAC AAC CAG AGG TAC GGC CTG AGC CCC GAC TAC TGG GGC CTT GGC	1872
	Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr Trp Gly Leu Gly	
	610 615 620	
60	TGC CTC ATC TAT GAG ATG ATC GAG GGC CAG TCG CCG TTC CGC GGC CGT	1920
	Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro Phe Arg Gly Arg	
	625 630 635 640	
65	AAG GAG AAG GTG AAG CGG GAG GAG GTG GAC CGC CGG GTC CTG GAG ACG	1968
	Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg Val Leu Glu Thr	
	645 650 655	

79

	GAG GAG GTG TAC TCC CAC AAG TTC TCC GAG GAG GCC AAG TCC ATC TGC	2016
	Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala Lys Ser Ile Cys	
	660 665 670	
5	AAG ATG CTG CTC ACG AAA GAT GCG AAG CAG AGG CTG GGC TGC CAG GAG	2064
	Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu Gly Cys Gln Glu	
	675 680 685	
10	GAG GGG GCT GCA GAG GTC AAG AGA CAC CCC TTC TTC AGG AAC ATG AAC	2112
	Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe Arg Asn Met Asn	
	690 695 700	
15	TTC AAG CGC TTA GAA GCC GGG ATG TTG GAC CCT CCC TTC GTT CCA GAC	2160
	Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro Phe Val Pro Asp	
	705 710 715 720	
20	CCC CGC GCT GTG TAC TGT AAG GAC GTG CTG GAC ATC GAG CAG TTC TCC	2208
	Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile Glu Gln Phe Ser	
	725 730 735	
	ACT GTG AAG GGC GTC AAT CTG GAC CAC ACA GAC GAC GAC TTC TAC TCC	2256
	Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp Asp Phe Tyr Ser	
	740 745 750	
25	AAG TTC TCC ACG GGC TCT GTG TCC ATC CCA TGG CAA AAC GAG ATG ATA	2304
	Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln Asn Glu Met Ile	
	755 760 765	
30	GAA ACA GAA TGC TTT AAG GAG CTG AAC GTG TTT GGA CCT AAT GGT ACC	2352
	Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly Pro Asn Gly Thr	
	770 775 780	
35	CTC CCG CCA GAT CTG AAC AGA AAC CAC CCT CCG GAA CCG CCC AAG AAA	2400
	Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu Pro Pro Lys Lys	
	785 790 795 800	
40	GGG CTG CTC CAG AGA CTC TTC AAG CGG CAG CAT CAG AAC AAT TCC AAG	2448
	Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln Asn Asn Ser Lys	
	805 810 815	
	AGT TCG CCC AGC TCC AAG ACC AGT TTT AAC CAC CAC ATA AAC TCA AAC	2496
	Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His Ile Asn Ser Asn	
	820 825 830	
45	CAT GTC AGC TCG AAC TCC ACC GGA AGC AGC TAG	2529
	His Val Ser Ser Asn Ser Thr Gly Ser Ser	
	835 840	

50 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 amino acids

(B) TYPE: amino acid

55 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1           5           10           15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
10           20           25           30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
           35           40           45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
           50           55           60
15 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
           65           70           75           80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
           85           90           95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
20           100          105          110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
           115          120          125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
           130          135          140
25 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
           145          150          155          160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
           165          170          175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
30           180          185          190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
           195          200          205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
           210          215          220
35 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
           225          230          235          240
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu
           245          250          255
Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly Gly
40           260          265          270
Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe
           275          280          285
Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr Ile Asp Arg Asp
           290          295          300
45 Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg Leu Leu Phe Arg
           305          310          315          320
Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr Ile Gln Phe Leu
           325          330          335
Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu Lys Leu Gly Glu
50           340          345          350
Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro Lys Ser Pro Val
           355          360          365
Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln Thr Glu Glu Lys
           370          375          380
55 Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala Cys Ala Gln Ser
           385          390          395          400

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81

	Val	His	Glu	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	His	Glu	Tyr	Leu	Asp	Ser
					405					410					415	
	Met	Phe	Phe	Asp	Arg	Phe	Leu	Gln	Trp	Lys	Trp	Leu	Glu	Arg	Gln	Pro
				420					425					430		
5	Val	Thr	Lys	Asn	Thr	Phe	Arg	Gln	Tyr	Arg	Val	Leu	Gly	Lys	Gly	Gly
			435					440					445			
	Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala	Thr	Gly	Lys	Met	Tyr
		450					455					460				
	Ala	Cys	Lys	Arg	Leu	Glu	Lys	Lys	Arg	Ile	Lys	Lys	Arg	Lys	Gly	Glu
10	465					470				475						480
	Ser	Met	Ala	Leu	Asn	Glu	Lys	Gln	Ile	Leu	Glu	Lys	Val	Asn	Ser	Gln
					485					490					495	
	Phe	Val	Val	Asn	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr	Lys	Asp	Ala	Leu	Cys
				500					505					510		
15	Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Gly	Asp	Leu	Lys	Phe	His	Ile	Tyr
			515					520					525			
	Asn	Met	Gly	Asn	Pro	Gly	Phe	Glu	Glu	Glu	Arg	Ala	Leu	Phe	Tyr	Ala
		530					535					540				
	Ala	Glu	Ile	Leu	Cys	Gly	Leu	Glu	Asp	Leu	His	Arg	Glu	Asn	Thr	Val
20	545					550					555					560
	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	Asp	Tyr	Gly	His
					565					570					575	
	Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Val	Lys	Ile	Pro	Glu	Gly	Asp
				580					585					590		
25	Leu	Ile	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr	Met	Ala	Pro	Glu	Val
			595				600						605			
	Leu	Asn	Asn	Gln	Arg	Tyr	Gly	Leu	Ser	Pro	Asp	Tyr	Trp	Gly	Leu	Gly
		610					615					620				
	Cys	Leu	Ile	Tyr	Glu	Met	Ile	Glu	Gly	Gln	Ser	Pro	Phe	Arg	Gly	Arg
30	625					630					635					640
	Lys	Glu	Lys	Val	Lys	Arg	Glu	Glu	Val	Asp	Arg	Arg	Val	Leu	Glu	Thr
					645					650					655	
	Glu	Glu	Val	Tyr	Ser	His	Lys	Phe	Ser	Glu	Glu	Ala	Lys	Ser	Ile	Cys
				660					665					670		
35	Lys	Met	Leu	Leu	Thr	Lys	Asp	Ala	Lys	Gln	Arg	Leu	Gly	Cys	Gln	Glu
			675					680					685			
	Glu	Gly	Ala	Ala	Glu	Val	Lys	Arg	His	Pro	Phe	Phe	Arg	Asn	Met	Asn
		690					695					700				
	Phe	Lys	Arg	Leu	Glu	Ala	Gly	Met	Leu	Asp	Pro	Pro	Phe	Val	Pro	Asp
40	705					710					715					720
	Pro	Arg	Ala	Val	Tyr	Cys	Lys	Asp	Val	Leu	Asp	Ile	Glu	Gln	Phe	Ser
					725					730					735	
	Thr	Val	Lys	Gly	Val	Asn	Leu	Asp	His	Thr	Asp	Asp	Asp	Phe	Tyr	Ser
				740					745					750		
45	Lys	Phe	Ser	Thr	Gly	Ser	Val	Ser	Ile	Pro	Trp	Gln	Asn	Glu	Met	Ile
			755					760					765			
	Glu	Thr	Glu	Cys	Phe	Lys	Glu	Leu	Asn	Val	Phe	Gly	Pro	Asn	Gly	Thr
		770					775					780				
	Leu	Pro	Pro	Asp	Leu	Asn	Arg	Asn	His	Pro	Pro	Glu	Pro	Pro	Lys	Lys
50	785					790					795					800
	Gly	Leu	Leu	Gln	Arg	Leu	Phe	Lys	Arg	Gln	His	Gln	Asn	Asn	Ser	Lys
					805					810					815	
	Ser	Ser	Pro	Ser	Ser	Lys	Thr	Ser	Phe	Asn	His	His	Ile	Asn	Ser	Asn
				820					825					830		
55	His	Val	Ser	Ser	Asn	Ser	Thr	Gly	Ser	Ser						
				835				840								

81

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1902 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 15 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1899
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

20	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
60	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
65	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	

83

	145	150	155	160	
5	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165	170	175	528
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190	576
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	195	200	205	624
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220	672
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	225	230	235	720
30	GGA CTC AGA TCT CGA GCT CGA GCC ATC ATG AGC AGA AGC AAG CGT GAC Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp	245	250	255	768
35	AAC AAT TTT TAT AGT GTA GAG ATT GGA GAT TCT ACA TTC ACA GTC CTG Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu	260	265	270	816
40	AAA CGA TAT CAG AAT TTA AAA CCT ATA GGC TCA GGA GCT CAA GGA ATA Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile	275	280	285	864
45	GTA TGC GCA GCT TAT GAT GCC ATT CTT GAA AGA AAT GTT GCA ATC AAG Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys	290	295	300	912
50	AAG CTA AGC CGA CCA TTT CAG AAT CAG ACT CAT GCC AAG CGG GCC TAC Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr	305	310	315	960
55	AGA GAG CTA GTT CTT ATG AAA TGT GTT AAT CAC AAA AAT ATA ATT GGC Arg Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Gly	325	330	335	1008
60	CTT TTG AAT GTT TTC ACA CCA CAG AAA TCC CTA GAA GAA TTT CAA GAT Leu Leu Asn Val Phe Thr Pro Gln Lys Ser Leu Glu Glu Phe Gln Asp	340	345	350	1056
65	GTT TAC ATA GTC ATG GAG CTC ATG GAT GCA AAT CTT TGC CAA GTG ATT Val Tyr Ile Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile	355	360	365	1104
70	CAG ATG GAG CTA GAT CAT GAA AGA ATG TCC TAC CTT CTC TAT CAG ATG Gln Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met				1152

84

	370	375	380	
5	CTG TGT GGA ATC AAG CAC CTT CAT TCT GCT GGA ATT ATT CAT CGG GAC Leu Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp 385 390 395 400	1200		
10	TTA AAG CCC AGT AAT ATA GTA GTA AAA TCT GAT TGC ACT TTG AAG ATT Leu Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile 405 410 415	1248		
15	CTT GAC TTC GGT CTG GCC AGG ACT GCA GGA ACG AGT TTT ATG ATG ACG Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr 420 425 430	1296		
20	CCT TAT GTA GTG ACT CGC TAC TAC AGA GCA CCC GAG GTC ATC CTT GGC Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly 435 440 445	1344		
25	ATG GGC TAC AAG GAA AAC GTG GAT TTA TGG TCT GTG GGG TGC ATT ATG Met Gly Tyr Lys Glu Asn Val Asp Leu Trp Ser Val Gly Cys Ile Met 450 455 460	1392		
30	GGA GAA ATG GTT TGC CAC AAA ATC CTC TTT CCA GGA AGG GAC TAT ATT Gly Glu Met Val Cys His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile 465 470 475 480	1440		
35	GAT CAG TGG AAT AAA GTT ATT GAA CAG CTT GGA ACA CCA TGT CCT GAA Asp Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu 485 490 495	1488		
40	TTC ATG AAG AAA CTG CAA CCA ACA GTA AGG ACT TAC GTT GAA AAC AGA Phe Met Lys Lys Leu Gln Pro Thr Val Arg Thr Tyr Val Glu Asn Arg 500 505 510	1536		
45	CCT AAA TAT GCT GGA TAT AGC TTT GAG AAA CTC TTC CCT GAT GTC CTT Pro Lys Tyr Ala Gly Tyr Ser Phe Glu Lys Leu Phe Pro Asp Val Leu 515 520 525	1584		
50	TTC CCA GCT GAC TCA GAA CAC AAC AAA CTT AAA GCC AGT CAG GCA AGG Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg 530 535 540	1632		
55	GAT TTG TTA TCC AAA ATG CTG GTA ATA GAT GCA TCT AAA AGG ATC TCT Asp Leu Leu Ser Lys Met Leu Val Ile Asp Ala Ser Lys Arg Ile Ser 545 550 555 560	1680		
60	GTA GAT GAA GCT CTC CAA CAC CCG TAC ATC AAT GTC TGG TAT GAT CCT Val Asp Glu Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro 565 570 575	1728		
65	TCT GAA GCA GAA GCT CCA CCA CCA AAG ATC CCT GAC AAG CAG TTA GAT Ser Glu Ala Glu Ala Pro Pro Pro Lys Ile Pro Asp Lys Gln Leu Asp 580 585 590	1776		
70	GAA AGG GAA CAC ACA ATA GAA GAG TGG AAA GAA TTG ATA TAT AAG GAA Glu Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu 1824			

85

	595		600		605	
	GTT ATG GAC TTG GAG GAG AGA ACC AAG AAT GGA GTT ATA CGG GGG CAG					1872
	Val Met Asp Leu Glu Glu Arg Thr Lys Asn Gly Val Ile Arg Gly Gln					
5	610		615		620	
	CCC TCT CCT TTA GCA CAG GTG CAG CAG TGA					1902
	Pro Ser Pro Leu Ala Gln Val Gln Gln					
10	625		630			

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 633 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

25	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
35	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
40	115 120 125	
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
50	195 200 205	
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
55	Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp	
	245 250 255	

85

86

Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu
 260 265 270
 Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile
 275 280 285
 5 Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys
 290 295 300
 Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr
 305 310 315 320
 Arg Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Gly
 325 330 335
 10 Leu Leu Asn Val Phe Thr Pro Gln Lys Ser Leu Glu Glu Phe Gln Asp
 340 345 350
 Val Tyr Ile Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile
 355 360 365
 15 Gln Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met
 370 375 380
 Leu Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp
 385 390 395 400
 Leu Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile
 405 410 415
 20 Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr
 420 425 430
 Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly
 435 440 445
 25 Met Gly Tyr Lys Glu Asn Val Asp Leu Trp Ser Val Gly Cys Ile Met
 450 455 460
 Gly Glu Met Val Cys His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile
 465 470 475 480
 Asp Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu
 485 490 495
 30 Phe Met Lys Lys Leu Gln Pro Thr Val Arg Thr Tyr Val Glu Asn Arg
 500 505 510
 Pro Lys Tyr Ala Gly Tyr Ser Phe Glu Lys Leu Phe Pro Asp Val Leu
 515 520 525
 35 Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg
 530 535 540
 Asp Leu Leu Ser Lys Met Leu Val Ile Asp Ala Ser Lys Arg Ile Ser
 545 550 555 560
 Val Asp Glu Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro
 565 570 575
 40 Ser Glu Ala Glu Ala Pro Pro Pro Lys Ile Pro Asp Lys Gln Leu Asp
 580 585 590
 Glu Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu
 595 600 605
 45 Val Met Asp Leu Glu Glu Arg Thr Lys Asn Gly Val Ile Arg Gly Gln
 610 615 620
 Pro Ser Pro Leu Ala Gln Val Gln Gln
 625 630

50 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1824 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

86

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 5 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1821
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

10 ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

15 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

20 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

25 TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

30 CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

35 CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

40 CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

45 GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

50 ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

55 AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

50 GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

55 GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

88

					180					185					190					
5	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG			624	
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu				
			195					200					205							
10	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC			672	
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe				
		210					215					220								
15	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC			720	
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser				
		225				230					235					240				
20	GGA	CTC	AGA	TCT	CGA	GGG	AAA	ATG	TCT	CAG	GAG	AGG	CCC	ACG	TTC	TAC			768	
	Gly	Leu	Arg	Ser	Arg	Gly	Lys	Met	Ser	Gln	Glu	Arg	Pro	Thr	Phe	Tyr				
					245					250					255					
25	CGG	CAG	GAG	CTG	AAC	AAG	ACA	ATC	TGG	GAG	GTG	CCC	GAG	CGT	TAC	CAG			816	
	Arg	Gln	Glu	Leu	Asn	Lys	Thr	Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln				
					260				265					270						
30	AAC	CTG	TCT	CCA	GTG	GGC	TCT	GGC	GCC	TAT	GGC	TCT	GTG	TGT	GCT	GCT			864	
	Asn	Leu	Ser	Pro	Val	Gly	Ser	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala				
			275					280					285							
35	TTT	GAC	ACA	AAA	ACG	GGG	TTA	CGT	GTG	GCA	GTG	AAG	AAG	CTC	TCC	AGA			912	
	Phe	Asp	Thr	Lys	Thr	Gly	Leu	Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg				
		290					295					300								
40	CCA	TTT	CAG	TCC	ATC	ATT	CAT	GCG	AAA	AGA	ACC	TAC	AGA	GAA	CTG	CGG			960	
	Pro	Phe	Gln	Ser	Ile	Ile	His	Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg				
		305				310					315					320				
45	TTA	CTT	AAA	CAT	ATG	AAA	CAT	GAA	AAT	GTG	ATT	GGT	CTG	TTG	GAC	GTT			1008	
	Leu	Leu	Lys	His	Met	Lys	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val				
					325					330					335					
50	TTT	ACA	CCT	GCA	AGG	TCT	CTG	GAG	GAA	TTC	AAT	GAT	GTG	TAT	CTG	GTG			1056	
	Phe	Thr	Pro	Ala	Arg	Ser	Leu	Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val				
				340					345					350						
55	ACC	CAT	CTC	ATG	GGG	GCA	GAT	CTG	AAC	AAC	ATT	GTG	AAA	TGT	CAG	AAG			1104	
	Thr	His	Leu	Met	Gly	Ala	Asp	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys				
				355				360					365							
60	CTT	ACA	GAT	GAC	CAT	GTT	CAG	TTC	CTT	ATC	TAC	CAA	ATT	CTC	CGA	GGT			1152	
	Leu	Thr	Asp	Asp	His	Val	Gln	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly				
		370					375					380								
65	CTA	AAG	TAT	ATA	CAT	TCA	GCT	GAC	ATA	ATT	CAC	AGG	GAC	CTA	AAA	CCT			1200	
	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro				
		385				390					395					400				
70	AGT	AAT	CTA	GCT	GTG	AAT	GAA	GAC	TGT	GAG	CTG	AAG	ATT	CTG	GAT	TTT			1248	
	Ser	Asn	Leu	Ala	Val	Asn	Glu	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe				

88

89

	405	410	415	
5	GGA CTG GCT CGG CAC ACA GAT GAT GAA ATG ACA GGC TAC GTG GCC ACT Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val Ala Thr 420 425 430	1296		
10	AGG TGG TAC AGG GCT CCT GAG ATC ATG CTG AAC TGG ATG CAT TAC AAC Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His Tyr Asn 435 440 445	1344		
15	CAG ACA GTT GAT ATT TGG TCA GTG GGA TGC ATA ATG GCC GAG CTG TTG Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu Leu Leu 450 455 460	1392		
20	ACT GGA AGA ACA TTG TTT CCT GGT ACA GAC CAT ATT GAT CAG TTG AAG Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln Leu Lys 465 470 475 480	1440		
25	CTC ATT TTA AGA CTC GTT GGA ACC CCA GGG GCT GAG CTT TTG AAG AAA Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu Lys Lys 485 490 495	1488		
30	ATC TCC TCA GAG TCT GCA AGA AAC TAT ATT CAG TCT TTG ACT CAG ATG Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr Gln Met 500 505 510	1536		
35	CCG AAG ATG AAC TTT GCG AAT GTA TTT ATT GGT GCC AAT CCC CTG GCT Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro Leu Ala 515 520 525	1584		
40	GTC GAC TTG CTG GAG AAG ATG CTT GTA TTG GAC TCA GAT AAG AGA ATT Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys Arg Ile 530 535 540	1632		
45	ACA GCG GCC CAA GCC CTT GCA CAT GCC TAC TTT GCT CAG TAC CAC GAT Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr His Asp 545 550 555 560	1680		
50	CCT GAT GAT GAA CCA GTG GCC GAT CCT TAT GAT CAG TCC TTT GAA AGC Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe Glu Ser 565 570 575	1728		
55	AGG GAC CTC CTT ATA GAT GAG TGG AAA AGC CTG ACC TAT GAT GAA GTC Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp Glu Val 580 585 590	1776		
60	ATC AGC TTT GTG CCA CCA CCC CTT GAC CAA GAA GAG ATG GAG TCC TGA Ile Ser Phe Val Pro Pro Pro Leu Asp Gln Glu Glu Met Glu Ser 595 600 605	1824		

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

10 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
    1      5      10      15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
    20      25      30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
    35      40      45
15 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50      55      60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
    65      70      75      80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
    85      90      95
20 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
    100      105      110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
    115      120      125
25 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130      135      140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
    145      150      155      160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
    165      170      175
30 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
    180      185      190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
    195      200      205
35 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210      215      220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
    225      230      235      240
Gly Leu Arg Ser Arg Gly Lys Met Ser Gln Glu Arg Pro Thr Phe Tyr
    245      250      255
40 Arg Gln Glu Leu Asn Lys Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln
    260      265      270
Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala
    275      280      285
45 Phe Asp Thr Lys Thr Gly Leu Arg Val Ala Val Lys Lys Leu Ser Arg
    290      295      300
Pro Phe Gln Ser Ile Ile His Ala Lys Arg Thr Tyr Arg Glu Leu Arg
    305      310      315      320
Leu Leu Lys His Met Lys His Glu Asn Val Ile Gly Leu Leu Asp Val
    325      330      335
50 Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe Asn Asp Val Tyr Leu Val
    340      345      350
Thr His Leu Met Gly Ala Asp Leu Asn Asn Ile Val Lys Cys Gln Lys
    355      360      365
55 Leu Thr Asp Asp His Val Gln Phe Leu Ile Tyr Gln Ile Leu Arg Gly
    370      375      380

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91

Leu Lys Tyr Ile His Ser Ala Asp Ile Ile His Arg Asp Leu Lys Pro
 385 390 395 400
 Ser Asn Leu Ala Val Asn Glu Asp Cys Glu Leu Lys Ile Leu Asp Phe
 405 410 415
 5 Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val Ala Thr
 420 425 430
 Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His Tyr Asn
 435 440 445
 10 Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu Leu Leu
 450 455 460
 Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln Leu Lys
 465 470 475 480
 Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu Lys Lys
 485 490 495
 15 Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr Gln Met
 500 505 510
 Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro Leu Ala
 515 520 525
 20 Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys Arg Ile
 530 535 540
 Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr His Asp
 545 550 555 560
 Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe Glu Ser
 565 570 575
 25 Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp Glu Val
 580 585 590
 Ile Ser Phe Val Pro Pro Pro Leu Asp Gln Glu Glu Met Glu Ser
 595 600 605

30 (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2907 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2904

(D) OTHER INFORMATION:

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 50 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 55 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

91

92

	35						40							45					
5	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC		192	
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr			
	50						55					60							
10	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG		240	
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys			
	65					70					75					80			
15	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG		288	
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu			
					85					90					95				
20	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG		336	
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu			
				100					105					110					
25	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC		384	
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly			
			115					120					125						
30	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC		432	
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr			
		130					135					140							
35	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC		480	
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn			
						150					155					160			
40	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC		528	
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser			
					165				170						175				
45	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC		576	
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly			
				180				185						190					
50	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG		624	
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu			
			195					200					205						
55	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC		672	
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe			
		210					215					220							
60	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC		720	
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser			
		225				230				235						240			
65	GGA	CTC	AGA	TCT	ATG	AGT	GCT	GAG	GGG	TAC	CAG	TAC	AGA	GCG	CTG	TAT		768	
	Gly	Leu	Arg	Ser	Met	Ser	Ala	Glu	Gly	Tyr	Gln	Tyr	Arg	Ala	Leu	Tyr			
					245					250					255				
70	GAT	TAT	AAA	AAG	GAA	AGA	GAA	GAA	GAT	ATT	GAC	TTG	CAC	TTG	GGT	GAC		816	
	Asp	Tyr	Lys	Lys	Glu	Arg	Glu	Glu	Asp	Ile	Asp	Leu	His	Leu	Gly	Asp			

92

93

	260	265	270	
5	ATA TTG ACT GTG AAT AAA GGG TCC TTA GTA GCT CTT GGA TTC AGT GAT Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp 275 280 285	864		
10	GGA CAG GAA GCC AGG CCT GAA GAA ATT GGC TGG TTA AAT GGC TAT AAT Gly Gln Glu Ala Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn 290 295 300	912		
15	GAA ACC ACA GGG GAA AGG GGG GAC TTT CCG GGA ACT TAC GTA GAA TAT Glu Thr Thr Gly Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr 305 310 315 320	960		
20	ATT GGA AGG AAA AAA ATC TCG CCT CCC ACA CCA AAG CCC CGG CCA CCT Ile Gly Arg Lys Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro 325 330 335	1008		
25	CGG CCT CTT CCT GTT GCA CCA GGT TCT TCG AAA ACT GAA GCA GAT GTT Arg Pro Leu Pro Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val 340 345 350	1056		
30	GAA CAA CAA GCT TTG ACT CTC CCG GAT CTT GCA GAG CAG TTT GCC CCT Glu Gln Gln Ala Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro 355 360 365	1104		
35	CCT GAC ATT GCC CCG CCT CTT CTT ATC AAG CTC GTG GAA GCC ATT GAA Pro Asp Ile Ala Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu 370 375 380	1152		
40	AAG AAA GGT CTG GAA TGT TCA ACT CTA TAC AGA ACA CAG AGC TCC AGC Lys Lys Gly Leu Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser 385 390 395 400	1200		
45	AAC CTG GCA GAA TTA CGA CAG CTT CTT GAT TGT GAT ACA CCC TCC GTG Asn Leu Ala Glu Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val 405 410 415	1248		
50	GAC TTG GAA ATG ATC GAT GTG CAC GTT TTG GCT GAC GCT TTC AAA CGC Asp Leu Glu Met Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg 420 425 430	1296		
55	TAT CTC CTG GAC TTA CCA AAT CCT GTC ATT CCA GCA GCC GTT TAC AGT Tyr Leu Leu Asp Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser 435 440 445	1344		
60	GAA ATG ATT TCT TTA GCT CCA GAA GTA CAA AGC TCC GAA GAA TAT ATT Glu Met Ile Ser Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile 450 455 460	1392		
65	CAG CTA TTG AAG AAG CTT ATT AGG TCG CCT AGC ATA CCT CAT CAG TAT Gln Leu Leu Lys Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr 465 470 475 480	1440		
70	TGG CTT ACG CTT CAG TAT TTG TTA AAA CAT TTC TTC AAG CTC TCT CAA Trp Leu Thr Leu Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln	1488		

93

94

	485	490	495	
5	ACC TCC AGC AAA AAT CTG TTG AAT GCA AGA GTA CTC TCT GAA ATT TTC Thr Ser Ser Lys Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe 500 505 510	1536		
10	AGC CCT ATG CTT TTC AGA TTC TCA GCA GCC AGC TCT GAT AAT ACT GAA Ser Pro Met Leu Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu 515 520 525	1584		
15	AAC CTC ATA AAA GTT ATA GAA ATT TTA ATC TCA ACT GAA TGG AAT GAA Asn Leu Ile Lys Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu 530 535 540	1632		
20	CGA CAG CCT GCA CCA GCA CTG CCT CCT AAA CCA CCA AAA CCT ACT ACT Arg Gln Pro Ala Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr 545 550 555 560	1680		
25	GTA GCC AAC AAC GGT ATG AAT AAC AAT ATG TCC TTA CAA AAT GCT GAA Val Ala Asn Asn Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu 565 570 575	1728		
30	TGG TAC TGG GGA GAT ATC TCG AGG GAA GAA GTG AAT GAA AAA CTT CGA Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg 580 585 590	1776		
35	GAT ACA GCA GAC GGG ACC TTT TTG GTA CGA GAT GCG TCT ACT AAA ATG Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met 595 600 605	1824		
40	CAT GGT GAT TAT ACT CTT ACA CTA AGG AAA GGG GGA AAT AAC AAA TTA His Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu 610 615 620	1872		
45	ATC AAA ATA TTT CAT CGA GAT GGG AAA TAT GGC TTC TCT GAC CCA TTA Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu 625 630 635 640	1920		
50	ACC TTC AGT TCT GTG GTT GAA TTA ATA AAC CAC TAC CGG AAT GAA TCT Thr Phe Ser Ser Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser 645 650 655	1968		
55	CTA GCT CAG TAT AAT CCC AAA TTG GAT GTG AAA TTA CTT TAT CCA GTA Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val 660 665 670	2016		
	TCC AAA TAC CAA CAG GAT CAA GTT GTC AAA GAA GAT AAT ATT GAA GCT Ser Lys Tyr Gln Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala 675 680 685	2064		
	GTA GGG AAA AAA TTA CAT GAA TAT AAC ACT CAG TTT CAA GAA AAA AGT Val Gly Lys Lys Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser 690 695 700	2112		
	CGA GAA TAT GAT AGA TTA TAT GAA GAA TAT ACC CGC ACA TCC CAG GAA Arg Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu	2160		

95

	705	710	715	720	
5	ATC CAA ATG AAA AGG ACA GCT ATT GAA GCA TTT AAT GAA ACC ATA AAA Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys	725	730	735	2208
10	ATA TTT GAA GAA CAG TGC CAG ACC CAA GAG CGG TAC AGC AAA GAA TAC Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr	740	745	750	2256
15	ATA GAA AAG TTT AAA CGT GAA GGC AAT GAG AAA GAA ATA CAA AGG ATT Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile	755	760	765	2304
20	ATG CAT AAT TAT GAT AAG TTG AAG TCT CGA ATC AGT GAA ATT ATT GAC Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp	770	775	780	2352
25	AGT AGA AGA AGA TTG GAA GAA GAC TTG AAG AAG CAG GCA GCT GAG TAT Ser Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr	785	790	795	2400
30	CGA GAA ATT GAC AAA CGT ATG AAC AGC ATT AAA CCA GAC CTT ATC CAG Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln	805	810	815	2448
35	CTG AGA AAG ACG AGA GAC CAA TAC TTG ATG TGG TTG ACT CAA AAA GGT Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly	820	825	830	2496
40	GTT CGG CAA AAG AAG TTG AAC GAG TGG TTG GGC AAT GAA AAC ACT GAA Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu	835	840	845	2544
45	GAC CAA TAT TCA CTG GTG GAA GAT GAT GAA GAT TTG CCC CAT CAT GAT Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp	850	855	860	2592
50	GAG AAG ACA TGG AAT GTT GGA AGC AGC AAC CGA AAC AAA GCT GAA AAC Glu Lys Thr Trp Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn	865	870	875	2640
55	CTG TTG CGA GGG AAG CGA GAT GGC ACT TTT CTT GTC CGG GAG AGC AGT Leu Leu Arg Gly Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser	885	890	895	2688
60	AAA CAG GGC TGC TAT GCC TGC TCT GTA GTG GTG GAC GGC GAA GTA AAG Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys	900	905	910	2736
65	CAT TGT GTC ATA AAC AAA ACA GCA ACT GGC TAT GGC TTT GCC GAG CCC His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro	915	920	925	2784
70	TAT AAC TTG TAC AGC TCT CTG AAA GAA CTG GTG CTA CAT TAC CAA CAC Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His				2832

95

96

930 935 940

ACC TCC CTT GTG CAG CAC AAC GAC TCC CTC AAT GTC ACA CTA GCC TAC 2880
 Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr
 5 945 950 955 960

CCA GTA TAT GCA CAG CAG AGG CGA TGA 2907
 Pro Val Tyr Ala Gln Gln Arg Arg
 965

10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 968 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

25 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 30 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 35 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 40 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 45 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 50 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 55 Gly Leu Arg Ser Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr
 245 250 255

96

97

	Asp	Tyr	Lys	Lys	Glu	Arg	Glu	Glu	Asp	Ile	Asp	Leu	His	Leu	Gly	Asp
				260					265					270		
	Ile	Leu	Thr	Val	Asn	Lys	Gly	Ser	Leu	Val	Ala	Leu	Gly	Phe	Ser	Asp
			275					280					285			
5	Gly	Gln	Glu	Ala	Arg	Pro	Glu	Glu	Ile	Gly	Trp	Leu	Asn	Gly	Tyr	Asn
		290					295					300				
	Glu	Thr	Thr	Gly	Glu	Arg	Gly	Asp	Phe	Pro	Gly	Thr	Tyr	Val	Glu	Tyr
	305					310					315				320	
	Ile	Gly	Arg	Lys	Lys	Ile	Ser	Pro	Pro	Thr	Pro	Lys	Pro	Arg	Pro	Pro
10					325					330					335	
	Arg	Pro	Leu	Pro	Val	Ala	Pro	Gly	Ser	Ser	Lys	Thr	Glu	Ala	Asp	Val
				340					345					350		
	Glu	Gln	Gln	Ala	Leu	Thr	Leu	Pro	Asp	Leu	Ala	Glu	Gln	Phe	Ala	Pro
			355					360					365			
15	Pro	Asp	Ile	Ala	Pro	Pro	Leu	Leu	Ile	Lys	Leu	Val	Glu	Ala	Ile	Glu
		370					375					380				
	Lys	Lys	Gly	Leu	Glu	Cys	Ser	Thr	Leu	Tyr	Arg	Thr	Gln	Ser	Ser	Ser
	385					390					395					400
	Asn	Leu	Ala	Glu	Leu	Arg	Gln	Leu	Leu	Asp	Cys	Asp	Thr	Pro	Ser	Val
20					405						410				415	
	Asp	Leu	Glu	Met	Ile	Asp	Val	His	Val	Leu	Ala	Asp	Ala	Phe	Lys	Arg
				420					425					430		
	Tyr	Leu	Leu	Asp	Leu	Pro	Asn	Pro	Val	Ile	Pro	Ala	Ala	Val	Tyr	Ser
		435					440					445				
25	Glu	Met	Ile	Ser	Leu	Ala	Pro	Glu	Val	Gln	Ser	Ser	Glu	Glu	Tyr	Ile
		450					455					460				
	Gln	Leu	Leu	Lys	Lys	Leu	Ile	Arg	Ser	Pro	Ser	Ile	Pro	His	Gln	Tyr
	465					470					475				480	
	Trp	Leu	Thr	Leu	Gln	Tyr	Leu	Leu	Lys	His	Phe	Phe	Lys	Leu	Ser	Gln
30					485					490					495	
	Thr	Ser	Ser	Lys	Asn	Leu	Leu	Asn	Ala	Arg	Val	Leu	Ser	Glu	Ile	Phe
				500					505					510		
	Ser	Pro	Met	Leu	Phe	Arg	Phe	Ser	Ala	Ala	Ser	Ser	Asp	Asn	Thr	Glu
			515					520					525			
35	Asn	Leu	Ile	Lys	Val	Ile	Glu	Ile	Leu	Ile	Ser	Thr	Glu	Trp	Asn	Glu
		530					535					540				
	Arg	Gln	Pro	Ala	Pro	Ala	Leu	Pro	Pro	Lys	Pro	Pro	Lys	Pro	Thr	Thr
	545					550					555				560	
	Val	Ala	Asn	Asn	Gly	Met	Asn	Asn	Asn	Met	Ser	Leu	Gln	Asn	Ala	Glu
40					565					570					575	
	Trp	Tyr	Trp	Gly	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu	Lys	Leu	Arg
			580						585				590			
	Asp	Thr	Ala	Asp	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala	Ser	Thr	Lys	Met
			595					600					605			
45	His	Gly	Asp	Tyr	Thr	Leu	Thr	Leu	Arg	Lys	Gly	Gly	Asn	Asn	Lys	Leu
		610					615					620				
	Ile	Lys	Ile	Phe	His	Arg	Asp	Gly	Lys	Tyr	Gly	Phe	Ser	Asp	Pro	Leu
	625					630					635				640	
	Thr	Phe	Ser	Ser	Val	Val	Glu	Leu	Ile	Asn	His	Tyr	Arg	Asn	Glu	Ser
50					645					650					655	
	Leu	Ala	Gln	Tyr	Asn	Pro	Lys	Leu	Asp	Val	Lys	Leu	Leu	Tyr	Pro	Val
				660					665					670		
	Ser	Lys	Tyr	Gln	Gln	Asp	Gln	Val	Val	Lys	Glu	Asp	Asn	Ile	Glu	Ala
			675					680					685			
55	Val	Gly	Lys	Lys	Leu	His	Glu	Tyr	Asn	Thr	Gln	Phe	Gln	Glu	Lys	Ser
		690					695					700				

97

98

Arg Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu
 705 710 715 720
 Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys
 725 730 735
 5 Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr
 740 745 750
 Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile
 755 760 765
 10 Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp
 770 775 780
 Ser Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr
 785 790 795 800
 Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln
 805 810 815
 15 Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly
 820 825 830
 Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu
 835 840 845
 20 Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp
 850 855 860
 Glu Lys Thr Trp Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn
 865 870 875 880
 Leu Leu Arg Gly Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser
 885 890 895
 25 Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys
 900 905 910
 His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro
 915 920 925
 30 Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His
 930 935 940
 Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr
 945 950 955 960
 Pro Val Tyr Ala Gln Gln Arg Arg
 965

35

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2157
 (D) OTHER INFORMATION:

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

55

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

48

99

	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
5	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
10	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
15	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75						80	
20	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTG	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
25	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
30	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
35	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
40	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
45	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170						175		
50	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185					190				
55	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
60	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
65	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	

100

	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG ACC ATG TCG TCC ATC	768
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ser Ser Ile	
	245 250 255	
5	TTG CCA TTC ACG CCG CCA GTT GTG AAG AGA CTG CTG GGA TGG AAG AAG	816
	Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys	
	260 265 270	
10	TCA GCT GGT GGG TCT GGA GGA GCA GGC GGA GGA GAG CAG AAT GGG CAG	864
	Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu Gln Asn Gly Gln	
	275 280 285	
15	GAA GAA AAG TGG TGT GAG AAA GCA GTG AAA AGT CTG GTG AAG AAG CTA	912
	Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu	
	290 295 300	
20	AAG AAA ACA GGA CGA TTA GAT GAG CTT GAG AAA GCC ATC ACC ACT CAA	960
	Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln	
	305 310 315 320	
25	AAC TGT AAT ACT AAA TGT GTT ACC ATA CCA AGC ACT TGC TCT GAA ATT	1008
	Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile	
	325 330 335	
30	TGG GGA CTG AGT ACA CCA AAT ACG ATA GAT CAG TGG GAT ACA ACA GGC	1056
	Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly	
	340 345 350	
35	CTT TAC AGC TTC TCT GAA CAA ACC AGG TCT CTT GAT GGT CGT CTC CAG	1104
	Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln	
	355 360 365	
40	GTA TCC CAT CGA AAA GGA TTG CCA CAT GTT ATA TAT TGC CGA TTA TGG	1152
	Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp	
	370 375 380	
45	CGC TGG CCT GAT CTT CAC AGT CAT CAT GAA CTC AAG GCA ATT GAA AAC	1200
	Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn	
	385 390 395 400	
50	TGC GAA TAT GCT TTT AAT CTT AAA AAG GAT GAA GTA TGT GTA AAC CCT	1248
	Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro	
	405 410 415	
55	TAC CAC TAT CAG AGA GTT GAG ACA CCA GTT TTG CCT CCA GTA TTA GTG	1296
	Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val	
	420 425 430	
60	CCC CGA CAC ACC GAG ATC CTA ACA GAA CTT CCG CCT CTG GAT GAC TAT	1344
	Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr	
	435 440 445	
65	ACT CAC TCC ATT CCA GAA AAC ACT AAC TTC CCA GCA GGA ATT GAG CCA	1392
	Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro	
	450 455 460	

100

101

	CAG AGT AAT TAT ATT CCA GAA ACG CCA CCT CCT GGA TAT ATC AGT GAA	1440
	Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu	
	465 470 475 480	
5	GAT GGA GAA ACA AGT GAC CAA CAG TTG AAT CAA AGT ATG GAC ACA GGC	1488
	Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly	
	485 490 495	
10	TCT CCA GCA GAA CTA TCT CCT ACT ACT CTT TCC CCT GTT AAT CAT AGC	1536
	Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser	
	500 505 510	
15	TTG GAT TTA CAG CCA GTT ACT TAC TCA GAA CCT GCA TTT TGG TGT TCA	1584
	Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser	
	515 520 525	
20	ATA GCA TAT TAT GAA TTA AAT CAG AGG GTT GGA GAA ACC TTC CAT GCA	1632
	Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala	
	530 535 540	
25	TCA CAG CCC TCA CTC ACT GTA GAT GGC TTT ACA GAC CCA TCA AAT TCA	1680
	Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser	
	545 550 555 560	
30	GAG AGG TTC TGC TTA GGT TTA CTC TCC AAT GTT AAC CGA AAT GCC ACG	1728
	Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr	
	565 570 575	
35	GTA GAA ATG ACA AGA AGG CAT ATA GGA AGA GGA GTG CGC TTA TAC TAC	1776
	Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr	
	580 585 590	
40	ATA GGT GGG GAA GTT TTT GCT GAG TGC CTA AGT GAT AGT GCA ATC TTT	1824
	Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe	
	595 600 605	
45	GTG CAG AGC CCC AAT TGT AAT CAG AGA TAT GGC TGG CAC CCT GCA ACA	1872
	Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr	
	610 615 620	
50	GTG TGT AAA ATT CCA CCA GGC TGT AAT CTG AAG ATC TTC AAC AAC CAG	1920
	Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln	
	625 630 635 640	
55	GAA TTT GCT GCT CTT CTG GCT CAG TCT GTT AAT CAG GGT TTT GAA GCC	1968
	Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala	
	645 650 655	
60	GTC TAT CAG CTA ACT AGA ATG TGC ACC ATA AGA ATG AGT TTT GTG AAA	2016
	Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys	
	660 665 670	
65	GGG TGG GGA GCA GAA TAC CGA AGG CAG ACG GTA ACA AGT ACT CCT TGC	2064
	Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys	
	675 680 685	

102

TGG ATT GAA CTT CAT CTG AAT GGA CCT CTA CAG TGG TTG GAC AAA GTA 2112
 Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val
 690 695 700

5 TTA ACT CAG ATG GGA TCC CCT TCA GTG CGT TGC TCA AGC ATG TCA TAA 2160
 Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
 705 710 715

10 (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 25 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 30 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 35 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 40 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 45 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 50 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ser Ser Ile
 245 250 255
 55 Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys
 260 265 270

102

103

	Ser	Ala	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Glu	Gln	Asn	Gly	Gln	
			275					280					285				
	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu	Val	Lys	Lys	Leu	
			290				295					300					
5	Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala	Ile	Thr	Thr	Gln	
			305			310					315					320	
	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr	Cys	Ser	Glu	Ile	
					325					330					335		
10	Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp	Asp	Thr	Thr	Gly	
				340					345					350			
	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp	Gly	Arg	Leu	Gln	
			355					360					365				
	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr	Cys	Arg	Leu	Trp	
			370				375					380					
15	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys	Ala	Ile	Glu	Asn	
						390					395					400	
	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val	Cys	Val	Asn	Pro	
					405					410					415		
20	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro	Pro	Val	Leu	Val	
				420					425					430			
	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro	Leu	Asp	Asp	Tyr	
			435					440					445				
	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala	Gly	Ile	Glu	Pro	
			450				455				460						
25	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly	Tyr	Ile	Ser	Glu	
						470					475					480	
	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser	Met	Asp	Thr	Gly	
					485				490					495			
30	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro	Val	Asn	His	Ser	
				500					505					510			
	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala	Phe	Trp	Cys	Ser	
			515					520					525				
	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu	Thr	Phe	His	Ala	
			530				535					540					
35	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp	Pro	Ser	Asn	Ser	
						550					555					560	
	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn	Arg	Asn	Ala	Thr	
					565					570					575		
40	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val	Arg	Leu	Tyr	Tyr	
				580					585					590			
	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp	Ser	Ala	Ile	Phe	
			595					600					605				
	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp	His	Pro	Ala	Thr	
			610				615					620					
45	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile	Phe	Asn	Asn	Gln	
						630					635					640	
	Glu	Phe	Ala	Ala	Leu	Leu	Ala	Gln	Ser	Val	Asn	Gln	Gly	Phe	Glu	Ala	
					645					650					655		
50	Val	Tyr	Gln	Leu	Thr	Arg	Met	Cys	Thr	Ile	Arg	Met	Ser	Phe	Val	Lys	
				660					665					670			
	Gly	Trp	Gly	Ala	Glu	Tyr	Arg	Arg	Gln	Thr	Val	Thr	Ser	Thr	Pro	Cys	
			675					680					685				
	Trp	Ile	Glu	Leu	His	Leu	Asn	Gly	Pro	Leu	Gln	Trp	Leu	Asp	Lys	Val	
			690				695					700					
55	Leu	Thr	Gln	Met	Gly	Ser	Pro	Ser	Val	Arg	Cys	Ser	Ser	Met	Ser		
			705				710				715						

103

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2421 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2418

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

20	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
60	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
65	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	

105

	145		150		155		160	
5	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165		170		175		528
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180		185		190		576
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	195		200		205		624
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210		215		220		672
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	225		230		235		720
30	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG AAT TCA ACC ATG GAC Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Asn Ser Thr Met Asp	245		250		255		768
35	AAT ATG TCT ATT ACG AAT ACA CCA ACA AGT AAT GAT GCC TGT CTG AGC Asn Met Ser Ile Thr Asn Thr Pro Thr Ser Asn Asp Ala Cys Leu Ser	260		265		270		816
40	ATT GTG CAT AGT TTG ATG TGC CAT AGA CAA GGT GGA GAG AGT GAA ACA Ile Val His Ser Leu Met Cys His Arg Gln Gly Gly Glu Ser Glu Thr	275		280		285		864
45	TTT GCA AAA AGA GCA ATT GAA AGT TTG GTA AAG AAG CTG AAG GAG AAA Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys Glu Lys	290		295		300		912
50	AAA GAT GAA TTG GAT TCT TTA ATA ACA GCT ATA ACT ACA AAT GGA GCT Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn Gly Ala	305		310		315		960
55	CAT CCT AGT AAA TGT GTT ACC ATA CAG AGA ACA TTG GAT GGG AGG CTT His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly Arg Leu	325		330		335		1008
60	CAG GTG GCT GGT CGG AAA GGA TTT CCT CAT GTG ATC TAT GCC CGT CTC Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala Arg Leu	340		345		350		1056
65	TGG AGG TGG CCT GAT CTT CAC AAA AAT GAA CTA AAA CAT GTT AAA TAT Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val Lys Tyr	355		360		365		1104
70	TGT CAG TAT GCG TTT GAC TTA AAA TGT GAT AGT GTC TGT GTG AAT CCA Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val Asn Pro							1152

105

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	370	375	380	
5	TAT CAC TAC GAA CGA GTT GTA TCA CCT GGA ATT GAT CTC TCA GGA TTA Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser Gly Leu 385 390 395 400	1200		
10	ACA CTG CAG AGT AAT GCT CCA TCA AGT ATG ATG GTG AAG GAT GAA TAT Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp Glu Tyr 405 410 415	1248		
15	GTG CAT GAC TTT GAG GGA CAG CCA TCG TTG TCC ACT GAA GGA CAT TCA Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly His Ser 420 425 430	1296		
20	ATT CAA ACC ATC CAG CAT CCA CCA AGT AAT CGT GCA TCG ACA GAG ACA Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr Glu Thr 435 440 445	1344		
25	TAC AGC ACC CCA GCT CTG TTA GCC CCA TCT GAG TCT AAT GCT ACC AGC Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala Thr Ser 450 455 460	1392		
30	ACT GCC AAC TTT CCC AAC ATT CCT GTG GCT TCC ACA AGT CAG CCT GCC Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln Pro Ala 465 470 475 480	1440		
35	AGT ATA CTG GGG GGC AGC CAT AGT GAA GGA CTG TTG CAG ATA GCA TCA Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile Ala Ser 485 490 495	1488		
40	GGG CCT CAG CCA GGA CAG CAG CAG AAT GGA TTT ACT GGT CAG CCA GCT Gly Pro Gln Pro Gly Gln Gln Gln Asn Gly Phe Thr Gly Gln Pro Ala 500 505 510	1536		
45	ACT TAC CAT CAT AAC AGC ACT ACC ACC TGG ACT GGA AGT AGG ACT GCA Thr Tyr His His Asn Ser Thr Thr Thr Trp Thr Gly Ser Arg Thr Ala 515 520 525	1584		
50	CCA TAC ACA CCT AAT TTG CCT CAC CAC CAA AAC GGC CAT CTT CAG CAC Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu Gln His 530 535 540	1632		
55	CAC CCG CCT ATG CCG CCC CAT CCC GGA CAT TAC TGG CCT GTT CAC AAT His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val His Asn 545 550 555 560	1680		
60	GAG CTT GCA TTC CAG CCT CCC ATT TCC AAT CAT CCT GCT CCT GAG TAT Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro Glu Tyr 565 570 575	1728		
65	TGG TGT TCC ATT GCT TAC TTT GAA ATG GAT GTT CAG GTA GGA GAG ACA Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly Glu Thr 580 585 590	1776		
70	TTT AAG GTT CCT TCA AGC TGC CCT ATT GTT ACT GTT GAT GGA TAC GTG Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly Tyr Val 600 605 610 615	1824		

106

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	595	600	605	
5	GAC CCT TCT GGA GGA GAT CGC TTT TGT TTG GGT CAA CTC TCC AAT GTC Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser Asn Val 610 615 620	1872		
10	CAC AGG ACA GAA GCC ATT GAG AGA GCA AGG TTG CAC ATA GGC AAA GGT His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly Lys Gly 625 630 635 640	1920		
15	GTG CAG TTG GAA TGT AAA GGT GAA GGT GAT GTT TGG GTC AGG TGC CTT Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg Cys Leu 645 650 655	1968		
20	AGT GAC CAC GCG GTC TTT GTA CAG AGT TAC TAC TTA GAC AGA GAA GCT Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg Glu Ala 660 665 670	2016		
25	GGG CGT GCA CCT GGA GAT GCT GTT CAT AAG ATC TAC CCA AGT GCA TAT Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser Ala Tyr 675 680 685	2064		
30	ATA AAG GTC TTT GAT TTG CGT CAG TGT CAT CGA CAG ATG CAG CAG CAG Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln Gln Gln 690 695 700	2112		
35	GCG GCT ACT GCA CAA GCT GCA GCA GCT GCC CAG GCA GCA GCC GTG GCA Ala Ala Thr Ala Gln Ala Ala Ala Ala Ala Gln Ala Ala Ala Val Ala 705 710 715 720	2160		
40	GGA AAC ATC CCT GGC CCA GGA TCA GTA GGT GGA ATA GCT CCA GCT ATC Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro Ala Ile 725 730 735	2208		
45	AGT CTG TCA GCT GCT GCT GGA ATT GGT GTT GAT GAC CTT CGT CGC TTA Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg Arg Leu 740 745 750	2256		
50	TGC ATA CTC AGG ATG AGT TTT GTG AAA GGC TGG GGA CCG GAT TAC CCA Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp Tyr Pro 755 760 765	2304		
55	AGA CAG AGC ATC AAA GAA ACA CCT TGC TGG ATT GAA ATT CAC TTA CAC Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His Leu His 770 775 780	2352		
	CGG GCC CTC CAG CTC CTA GAC GAA GTA CTT CAT ACC ATG CCG ATT GCA Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro Ile Ala 785 790 795 800	2400		
	GAC CCA CAA CCT TTA GAC TGA Asp Pro Gln Pro Leu Asp 805	2421		

(2) INFORMATION FOR SEQ ID NO:53:

107

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 amino acids

(B) TYPE: amino acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
15	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35					40					45			
20	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70					75				80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
25	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
30		130					135					140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155				160		
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170					175			
35	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
40		210					215					220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
					230						235				240		
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Asn	Ser	Thr	Met	Asp	
				245					250					255			
45	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys	Leu	Ser	
				260					265					270			
	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser	Glu	Thr	
			275					280					285				
	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys	Glu	Lys	
50		290					295					300					
	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn	Gly	Ala	
	305					310					315				320		
	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly	Arg	Leu	
				325					330					335			
55	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala	Arg	Leu	
				340					345					350			

109

	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val	Lys	Tyr
			355					360					365			
	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val	Asn	Pro
		370					375					380				
5	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser	Gly	Leu
		385			390						395					400
	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp	Glu	Tyr
				405						410					415	
10	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly	His	Ser
				420						425				430		
	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr	Glu	Thr
			435					440					445			
	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala	Thr	Ser
		450					455					460				
15	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln	Pro	Ala
		465				470					475					480
	Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile	Ala	Ser
				485						490					495	
20	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln	Pro	Ala
			500						505					510		
	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg	Thr	Ala
		515						520					525			
	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu	Gln	His
		530					535					540				
25	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val	His	Asn
		545				550					555					560
	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro	Glu	Tyr
				565						570					575	
30	Trp	Cys	Ser	Ile	Ala	Tyr	Phe	Glu	Met	Asp	Val	Gln	Val	Gly	Glu	Thr
				580					585					590		
	Phe	Lys	Val	Pro	Ser	Ser	Cys	Pro	Ile	Val	Thr	Val	Asp	Gly	Tyr	Val
		595					600						605			
	Asp	Pro	Ser	Gly	Gly	Asp	Arg	Phe	Cys	Leu	Gly	Gln	Leu	Ser	Asn	Val
		610				615						620				
35	His	Arg	Thr	Glu	Ala	Ile	Glu	Arg	Ala	Arg	Leu	His	Ile	Gly	Lys	Gly
		625				630					635					640
	Val	Gln	Leu	Glu	Cys	Lys	Gly	Glu	Gly	Asp	Val	Trp	Val	Arg	Cys	Leu
				645						650					655	
40	Ser	Asp	His	Ala	Val	Phe	Val	Gln	Ser	Tyr	Tyr	Leu	Asp	Arg	Glu	Ala
			660						665					670		
	Gly	Arg	Ala	Pro	Gly	Asp	Ala	Val	His	Lys	Ile	Tyr	Pro	Ser	Ala	Tyr
		675					680						685			
	Ile	Lys	Val	Phe	Asp	Leu	Arg	Gln	Cys	His	Arg	Gln	Met	Gln	Gln	Gln
		690				695						700				
45	Ala	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Ala	Gln	Ala	Ala	Ala	Ala	Val	Ala
		705				710				715						720
	Gly	Asn	Ile	Pro	Gly	Pro	Gly	Ser	Val	Gly	Gly	Ile	Ala	Pro	Ala	Ile
				725						730					735	
50	Ser	Leu	Ser	Ala	Ala	Ala	Gly	Ile	Gly	Val	Asp	Asp	Leu	Arg	Arg	Leu
			740						745					750		
	Cys	Ile	Leu	Arg	Met	Ser	Phe	Val	Lys	Gly	Trp	Gly	Pro	Asp	Tyr	Pro
		755					760						765			
	Arg	Gln	Ser	Ile	Lys	Glu	Thr	Pro	Cys	Trp	Ile	Glu	Ile	His	Leu	His
		770					775					780				
55	Arg	Ala	Leu	Gln	Leu	Leu	Asp	Glu	Val	Leu	His	Thr	Met	Pro	Ile	Ala
		785				790					795					800

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Asp Pro Gln Pro Leu Asp
805

(2) INFORMATION FOR SEQ ID NO:54:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

15

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...3117

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

20

ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10						15		

25

GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

30

GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

35

TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						

40

CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	

45

CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90					95			

50

CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

55

GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140				

110

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	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
5	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165					170					175		
10	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
15	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
20	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
25	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235						240	
30	GGA	CTC	AGA	TCT	ACC	ATG	GCG	GGC	TGG	ATC	CAG	GCC	CAG	CAG	CTG	CAG	768
	Gly	Leu	Arg	Ser	Thr	Met	Ala	Gly	Trp	Ile	Gln	Ala	Gln	Gln	Leu	Gln	
					245					250					255		
35	GGA	GAC	GCG	CTG	CGC	CAG	ATG	CAG	GTG	CTG	TAC	GGC	CAG	CAC	TTC	CCC	816
	Gly	Asp	Ala	Leu	Arg	Gln	Met	Gln	Val	Leu	Tyr	Gly	Gln	His	Phe	Pro	
				260					265					270			
40	ATC	GAG	GTC	CGG	CAC	TAC	TTG	GCC	CAG	TGG	ATT	GAG	AGC	CAG	CCA	TGG	864
	Ile	Glu	Val	Arg	His	Tyr	Leu	Ala	Gln	Trp	Ile	Glu	Ser	Gln	Pro	Trp	
			275					280					285				
45	GAT	GCC	ATT	GAC	TTG	GAC	AAT	CCC	CAG	GAC	AGA	GCC	CAA	GCC	ACC	CAG	912
	Asp	Ala	Ile	Asp	Leu	Asp	Asn	Pro	Gln	Asp	Arg	Ala	Gln	Ala	Thr	Gln	
		290					295					300					
50	CTC	CTG	GAG	GGC	CTG	GTG	CAG	GAG	CTG	CAG	AAG	AAG	GCG	GAG	CAC	CAG	960
	Leu	Leu	Glu	Gly	Leu	Val	Gln	Glu	Leu	Gln	Lys	Lys	Ala	Glu	His	Gln	
	305					310					315					320	
55	GTG	GGG	GAA	GAT	GGG	TTT	TTA	CTG	AAG	ATC	AAG	CTG	GGG	CAC	TAC	GCC	1008
	Val	Gly	Glu	Asp	Gly	Phe	Leu	Leu	Lys	Ile	Lys	Leu	Gly	His	Tyr	Ala	
					325					330					335		
60	ACG	CAG	CTC	CAG	AAA	ACA	TAT	GAC	CGC	TGC	CCC	CTG	GAG	CTG	GTC	CGC	1056
	Thr	Gln	Leu	Gln	Lys	Thr	Tyr	Asp	Arg	Cys	Pro	Leu	Glu	Leu	Val	Arg	
				340					345					350			
65	TGC	ATC	CGG	CAC	ATT	CTG	TAC	AAT	GAA	CAG	AGG	CTG	GTC	CGA	GAA	GCC	1104
	Cys	Ile	Arg	His	Ile	Leu	Tyr	Asn	Glu	Gln	Arg	Leu	Val	Arg	Glu	Ala	
			355					360					365				

111

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	AAC AAT TGC AGC TCT CCG GCT GGG ATC CTG GTT GAC GCC ATG TCC CAG	1152
	Asn Asn Cys Ser Ser Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln	
	370 375 380	
5	AAG CAC CTT CAG ATC AAC CAG ACA TTT GAG GAG CTG CGA CTG GTC ACG	1200
	Lys His Leu Gln Ile Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr	
	385 390 395 400	
10	CAG GAC ACA GAG AAT GAG CTG AAG AAA CTG CAG CAG ACT CAG GAG TAC	1248
	Gln Asp Thr Glu Asn Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr	
	405 410 415	
15	TTC ATC ATC CAG TAC CAG GAG AGC CTG AGG ATC CAA GCT CAG TTT GCC	1296
	Phe Ile Ile Gln Tyr Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala	
	420 425 430	
20	CAG CTG GCC CAG CTG AGC CCC CAG GAG CGT CTG AGC CGG GAG ACG GCC	1344
	Gln Leu Ala Gln Leu Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala	
	435 440 445	
25	CTC CAG CAG AAG CAG GTG TCT CTG GAG GCC TGG TTG CAG CGT GAG GCA	1392
	Leu Gln Gln Lys Gln Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala	
	450 455 460	
30	CAG ACA CTG CAG CAG TAC CGC GTG GAG CTG GCC GAG AAG CAC CAG AAG	1440
	Gln Thr Leu Gln Gln Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys	
	465 470 475 480	
35	ACC CTG CAG CTG CTG CGG AAG CAG CAG ACC ATC ATC CTG GAT GAC GAG	1488
	Thr Leu Gln Leu Leu Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu	
	485 490 495	
40	CTG ATC CAG TGG AAG CGG CGG CAG CAG CTG GCC GGG AAC GGC GGG CCC	1536
	Leu Ile Gln Trp Lys Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro	
	500 505 510	
45	CCC GAG GGC AGC CTG GAC GTG CTA CAG TCC TGG TGT GAG AAG TTG GCC	1584
	Pro Glu Gly Ser Leu Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala	
	515 520 525	
50	GAG ATC ATC TGG CAG AAC CGG CAG CAG ATC CGC AGG GCT GAG CAC CTC	1632
	Glu Ile Ile Trp Gln Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu	
	530 535 540	
55	TGC CAG CAG CTG CCC ATC CCC GGC CCA GTG GAG GAG ATG CTG GCC GAG	1680
	Cys Gln Gln Leu Pro Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu	
	545 550 555 560	
60	GTC AAC GCC ACC ATC ACG GAC ATT ATC TCA GCC CTG GTG ACC AGC ACA	1728
	Val Asn Ala Thr Ile Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr	
	565 570 575	
65	TTC ATC ATT GAG AAG CAG CCT CCT CAG GTC CTG AAG ACC CAG ACC AAG	1776
	Phe Ile Ile Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys	
	580 585 590	

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	TTT	GCA	GCC	ACC	GTA	CGC	CTG	CTG	GTG	GGC	GGG	AAG	CTG	AAC	GTG	CAC	1824
	Phe	Ala	Ala	Thr	Val	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	
			595					600					605				
5	ATG	AAT	CCC	CCC	CAG	GTG	AAG	GCC	ACC	ATC	ATC	AGT	GAG	CAG	CAG	GCC	1872
	Met	Asn	Pro	Pro	Gln	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	
			610				615					620					
10	AAG	TCT	CTG	CTT	AAA	AAT	GAG	AAC	ACC	CGC	AAC	GAG	TGC	AGT	GGT	GAG	1920
	Lys	Ser	Leu	Leu	Lys	Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	
			625			630					635					640	
15	ATC	CTG	AAC	AAC	TGC	TGC	GTG	ATG	GAG	TAC	CAC	CAA	GCC	ACG	GGC	ACC	1968
	Ile	Leu	Asn	Asn	Cys	Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	
					645				650						655		
20	CTC	AGT	GCC	CAC	TTC	AGG	AAC	ATG	TCA	CTG	AAG	AGG	ATC	AAG	CGT	GCT	2016
	Leu	Ser	Ala	His	Phe	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	
				660					665					670			
25	GAC	CGG	CGG	GGT	GCA	GAG	TCC	GTG	ACA	GAG	GAG	AAG	TTC	ACA	GTC	CTG	2064
	Asp	Arg	Arg	Gly	Ala	Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	
				675				680					685				
30	TTT	GAG	TCT	CAG	TTC	AGT	GTT	GGC	AGC	AAT	GAG	CTT	GTG	TTC	CAG	GTG	2112
	Phe	Glu	Ser	Gln	Phe	Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	
				690			695					700					
35	AAG	ACT	CTG	TCC	CTA	CCT	GTG	GTT	GTC	ATC	GTC	CAC	GGC	AGC	CAG	GAC	2160
	Lys	Thr	Leu	Ser	Leu	Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	
						710					715				720		
40	CAC	AAT	GCC	ACG	GCT	ACT	GTG	CTG	TGG	GAC	AAT	GCC	TTT	GCT	GAG	CCG	2208
	His	Asn	Ala	Thr	Ala	Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	
					725					730					735		
45	GGC	AGG	GTG	CCA	TTT	GCC	GTG	CCT	GAC	AAA	GTG	CTG	TGG	CCG	CAG	CTG	2256
	Gly	Arg	Val	Pro	Phe	Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	
				740					745					750			
50	TGT	GAG	GCG	CTC	AAC	ATG	AAA	TTC	AAG	GCC	GAA	GTG	CAG	AGC	AAC	CGG	2304
	Cys	Glu	Ala	Leu	Asn	Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	
				755				760					765				
55	GGC	CTG	ACC	AAG	GAG	AAC	CTC	GTG	TTC	CTG	GCG	CAG	AAA	CTG	TTC	AAC	2352
	Gly	Leu	Thr	Lys	Glu	Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	
				770			775					780					
60	AAC	AGC	AGC	AGC	CAC	CTG	GAG	GAC	TAC	AGT	GGC	CTG	TCC	GTG	TCC	TGG	2400
	Asn	Ser	Ser	Ser	His	Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser	Trp	
						790					795					800	
65	TCC	CAG	TTC	AAC	AGG	GAG	AAC	TTG	CCG	GGC	TGG	AAC	TAC	ACC	TTC	TGG	2448
	Ser	Gln	Phe	Asn	Arg	Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	
					805					810					815		

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	CAG TGG TTT GAC GGG GTG ATG GAG GTG TTG AAG AAG CAC CAC AAG CCC	2496
	Gln Trp Phe Asp Gly Val Met Glu Val Leu Lys Lys His His Lys Pro	
	820 825 830	
5	CAC TGG AAT GAT GGG GCC ATC CTA GGT TTT GTG AAT AAG CAA CAG GCC	2544
	His Trp Asn Asp Gly Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala	
	835 840 845	
10	CAC GAC CTG CTC ATC AAC AAG CCC GAC GGG ACC TTC TTG TTG CGC TTT	2592
	His Asp Leu Leu Ile Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe	
	850 855 860	
15	AGT GAC TCA GAA ATC GGG GGC ATC ACC ATC GCC TGG AAG TTT GAC TCC	2640
	Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser	
	865 870 875 880	
20	CCG GAA CGC AAC CTG TGG AAC CTG AAA CCA TTC ACC ACG CGG GAT TTC	2688
	Pro Glu Arg Asn Leu Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe	
	885 890 895	
	TCC ATC AGG TCC CTG GCT GAC CGG CTG GGG GAC CTG AGC TAT CTC ATC	2736
	Ser Ile Arg Ser Leu Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile	
	900 905 910	
25	TAT GTG TTT CCT GAC CGC CCC AAG GAT GAG GTC TTC TCC AAG TAC TAC	2784
	Tyr Val Phe Pro Asp Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr	
	915 920 925	
30	ACT CCT GTG CTG GCT AAA GCT GTT GAT GGA TAT GTG AAA CCA CAG ATC	2832
	Thr Pro Val Leu Ala Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile	
	930 935 940	
35	AAG CAA GTG GTC CCT GAG TTT GTG AAT GCA TCT GCA GAT GCT GGG GGC	2880
	Lys Gln Val Val Pro Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly	
	945 950 955 960	
40	AGC AGC GCC ACG TAC ATG GAC CAG GCC CCC TCC CCA GCT GTG TGC CCC	2928
	Ser Ser Ala Thr Tyr Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro	
	965 970 975	
	CAG GCT CCC TAT AAC ATG TAC CCA CAG AAC CCT GAC CAT GTA CTC GAT	2976
	Gln Ala Pro Tyr Asn Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp	
	980 985 990	
45	CAG GAT GGA GAA TTC GAC CTG GAT GAG ACC ATG GAT GTG GCC AGG CAC	3024
	Gln Asp Gly Glu Phe Asp Leu Asp Glu Thr Met Asp Val Ala Arg His	
	995 1000 1005	
50	GTG GAG GAA CTC TTA CGC CGA CCA ATG GAC AGT CTT GAC TCC CGC CTC	3072
	Val Glu Glu Leu Leu Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu	
	1010 1015 1020	
55	TCG CCC CCT GCC GGT CTT TTC ACC TCT GCC AGA GGC TCC CTC TCA TGA	3120
	Ser Pro Pro Ala Gly Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser	
	1025 1030 1035 1	

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1039 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

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15 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
    1      5      10      15
    Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
      20      25      30
    Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
    20      35      40      45
    Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50      55      60
    Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
      65      70      75      80
    25 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
      85      90      95
    Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
      100      105      110
    Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
    30      115      120      125
    Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
      130      135      140
    Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
      145      150      155      160
    35 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
      165      170      175
    Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
      180      185      190
    Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
    40      195      200      205
    Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
      210      215      220
    Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
      225      230      235      240
    45 Gly Leu Arg Ser Thr Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln
      245      250      255
    Gly Asp Ala Leu Arg Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro
      260      265      270
    Ile Glu Val Arg His Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp
    50      275      280      285
    Asp Ala Ile Asp Leu Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln
      290      295      300
    Leu Leu Glu Gly Leu Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln
      305      310      315      320
    55 Val Gly Glu Asp Gly Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala
      325      330      335

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	Thr	Gln	Leu	Gln	Lys	Thr	Tyr	Asp	Arg	Cys	Pro	Leu	Glu	Leu	Val	Arg	
				340					345					350			
	Cys	Ile	Arg	His	Ile	Leu	Tyr	Asn	Glu	Gln	Arg	Leu	Val	Arg	Glu	Ala	
			355					360					365				
5	Asn	Asn	Cys	Ser	Ser	Pro	Ala	Gly	Ile	Leu	Val	Asp	Ala	Met	Ser	Gln	
			370				375					380					
	Lys	His	Leu	Gln	Ile	Asn	Gln	Thr	Phe	Glu	Glu	Leu	Arg	Leu	Val	Thr	
			385			390					395					400	
	Gln	Asp	Thr	Glu	Asn	Glu	Leu	Lys	Lys	Leu	Gln	Gln	Thr	Gln	Glu	Tyr	
10					405					410					415		
	Phe	Ile	Ile	Gln	Tyr	Gln	Glu	Ser	Leu	Arg	Ile	Gln	Ala	Gln	Phe	Ala	
				420					425					430			
	Gln	Leu	Ala	Gln	Leu	Ser	Pro	Gln	Glu	Arg	Leu	Ser	Arg	Glu	Thr	Ala	
			435					440					445				
15	Leu	Gln	Gln	Lys	Gln	Val	Ser	Leu	Glu	Ala	Trp	Leu	Gln	Arg	Glu	Ala	
			450				455					460					
	Gln	Thr	Leu	Gln	Gln	Tyr	Arg	Val	Glu	Leu	Ala	Glu	Lys	His	Gln	Lys	
			465			470					475					480	
	Thr	Leu	Gln	Leu	Leu	Arg	Lys	Gln	Gln	Thr	Ile	Ile	Leu	Asp	Asp	Glu	
20					485					490					495		
	Leu	Ile	Gln	Trp	Lys	Arg	Arg	Gln	Gln	Leu	Ala	Gly	Asn	Gly	Gly	Pro	
			500					505					510				
	Pro	Glu	Gly	Ser	Leu	Asp	Val	Leu	Gln	Ser	Trp	Cys	Glu	Lys	Leu	Ala	
			515					520					525				
25	Glu	Ile	Ile	Trp	Gln	Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu	
			530				535					540					
	Cys	Gln	Gln	Leu	Pro	Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu	
			545			550					555					560	
	Val	Asn	Ala	Thr	Ile	Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	
30					565					570					575		
	Phe	Ile	Ile	Glu	Lys	Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	
				580					585					590			
	Phe	Ala	Ala	Thr	Val	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	
			595				600					605					
35	Met	Asn	Pro	Pro	Gln	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	
			610				615					620					
	Lys	Ser	Leu	Leu	Lys	Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	
					625		630				635					640	
	Ile	Leu	Asn	Asn	Cys	Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	
40					645					650					655		
	Leu	Ser	Ala	His	Phe	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	
				660					665					670			
	Asp	Arg	Arg	Gly	Ala	Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	
			675					680					685				
45	Phe	Glu	Ser	Gln	Phe	Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	
			690				695					700					
	Lys	Thr	Leu	Ser	Leu	Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	
			705			710					715					720	
	His	Asn	Ala	Thr	Ala	Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	
50					725					730					735		
	Gly	Arg	Val	Pro	Phe	Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	
				740					745					750			
	Cys	Glu	Ala	Leu	Asn	Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	
			755					760					765				
55	Gly	Leu	Thr	Lys	Glu	Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	
			770				775						780				

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Asn Ser Ser Ser His Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp
 785 790 795 800
 Ser Gln Phe Asn Arg Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp
 805 810 815
 5 Gln Trp Phe Asp Gly Val Met Glu Val Leu Lys Lys His His Lys Pro
 820 825 830
 His Trp Asn Asp Gly Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala
 835 840 845
 10 His Asp Leu Leu Ile Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe
 850 855 860
 Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser
 865 870 875 880
 Pro Glu Arg Asn Leu Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe
 885 890 895
 15 Ser Ile Arg Ser Leu Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile
 900 905 910
 Tyr Val Phe Pro Asp Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr
 915 920 925
 20 Thr Pro Val Leu Ala Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile
 930 935 940
 Lys Gln Val Val Pro Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly
 945 950 955 960
 Ser Ser Ala Thr Tyr Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro
 965 970 975
 25 Gln Ala Pro Tyr Asn Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp
 980 985 990
 Gln Asp Gly Glu Phe Asp Leu Asp Glu Thr Met Asp Val Ala Arg His
 995 1000 1005
 30 Val Glu Glu Leu Leu Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu
 1010 1015 1020
 Ser Pro Pro Ala Gly Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser
 1025 1030 1035 1

(2) INFORMATION FOR SEQ ID NO:56:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1875 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

45

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1872
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

50

ATG GCG GCG GCG GCG GCG GCT CCG GGG GGC GGG GGC GGG GAG CCC AGG 48
 Met Ala Ala Ala Ala Ala Ala Pro Gly Gly Gly Gly Gly Glu Pro Arg
 1 5 10 15

55

GGA ACT GCT GGG GTC GTC CCG GTG GTC CCC GGG GAG GTG GAG GTG GTG 96
 Gly Thr Ala Gly Val Val Pro Val Val Pro Gly Glu Val Glu Val Val

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	20					25					30							
5	AAG	GGG	CAG	CCA	TTC	GAT	GTG	GGC	CCA	CGC	TAC	ACG	CAG	CTG	CAG	TAC	144	
	Lys	Gly	Gln	Pro	Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Gln	Leu	Gln	Tyr		
	35					40					45							
10	ATC	GGC	GAG	GGC	GCG	TAC	GGC	ATG	GTC	AGC	TCA	GCT	TAT	GAC	CAC	GTG	192	
	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Met	Val	Ser	Ser	Ala	Tyr	Asp	His	Val		
	50					55					60							
15	CGC	AAG	ACC	AGA	GTG	GCC	ATC	AAG	AAG	ATC	AGC	CCC	TTT	GAG	CAT	CAA	240	
	Arg	Lys	Thr	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln		
	65					70					75					80		
20	ACC	TAC	TGT	CAG	CGC	ACG	CTG	AGG	GAG	ATC	CAG	ATC	TTG	CTG	CGA	TTC	288	
	Thr	Tyr	Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Gln	Ile	Leu	Leu	Arg	Phe		
	85					90					95							
25	CGC	CAT	GAG	AAT	GTT	ATA	GGC	ATC	CGA	GAC	ATC	CTC	AGA	GCG	CCC	ACC	336	
	Arg	His	Glu	Asn	Val	Ile	Gly	Ile	Arg	Asp	Ile	Leu	Arg	Ala	Pro	Thr		
	100					105					110							
30	CTG	GAA	GCC	ATG	AGA	GAT	GTT	TAC	ATT	GTT	CAG	GAC	CTC	ATG	GAG	ACA	384	
	Leu	Glu	Ala	Met	Arg	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr		
	115					120					125							
35	GAC	CTG	TAC	AAG	CTG	CTT	AAA	AGC	CAG	CAG	CTG	AGC	AAT	GAC	CAC	ATC	432	
	Asp	Leu	Tyr	Lys	Leu	Leu	Lys	Ser	Gln	Gln	Leu	Ser	Asn	Asp	His	Ile		
	130					135					140							
40	TGC	TAC	TTC	CTC	TAC	CAG	ATC	CTC	CGG	GGC	CTC	AAG	TAT	ATA	CAC	TCA	480	
	Cys	Tyr	Phe	Leu	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser		
	145					150					155					160		
45	GCC	AAT	GTG	CTG	CAC	CGG	GAC	CTG	AAG	CCT	TCC	AAT	CTG	CTT	ATC	AAC	528	
	Ala	Asn	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Ile	Asn		
	165					170					175							
50	ACC	ACC	TGC	GAC	CTT	AAG	ATC	TGT	GAT	TTT	GGC	CTG	GCC	CGG	ATT	GCT	576	
	Thr	Thr	Cys	Asp	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ala		
	180					185					190							
55	GAC	CCT	GAG	CAC	GAC	CAC	ACT	GGC	TTT	CTG	ACG	GAG	TAT	GTG	GCC	ACA	624	
	Asp	Pro	Glu	His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr		
	195					200					205							
60	CGC	TGG	TAC	CGA	GCC	CCA	GAG	ATC	ATG	CTT	AAT	TCC	AAG	GGC	TAC	ACC	672	
	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr		
	210					215					220							
65	AAA	TCC	ATC	GAC	ATC	TGG	TCT	GTG	GGC	TGC	ATT	CTG	GCT	GAG	ATG	CTC	720	
	Lys	Ser	Ile	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu		
	225					230					235					240		
70	TCC	AAC	CGG	CCC	ATC	TTC	CCC	GGC	AAG	CAC	TAC	CTG	GAC	CAG	CTC	AAC	768	
	Ser	Asn	Arg	Pro	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn		

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	245								250				255					
5	CAC	ATT	CTA	GGT	ATC	TTG	GGT	TCC	CCA	TCC	CAG	GAG	GAC	CTT	AAT	TGC	816	
	His	Ile	Leu	Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys		
				260					265					270				
10	ATC	ATT	AAC	ATG	AAG	GCC	CGA	AAC	TAC	CTG	CAG	TCT	CTG	CCC	TCG	AAA	864	
	Ile	Ile	Asn	Met	Lys	Ala	Arg	Asn	Tyr	Leu	Gln	Ser	Leu	Pro	Ser	Lys		
				275				280					285					
15	ACC	AAG	GTG	GCT	TGG	GCC	AAG	CTC	TTT	CCT	AAA	TCT	GAC	TCC	AAA	GCT	912	
	Thr	Lys	Val	Ala	Trp	Ala	Lys	Leu	Phe	Pro	Lys	Ser	Asp	Ser	Lys	Ala		
				290			295					300						
20	CTT	GAC	CTG	CTG	GAC	CGG	ATG	TTA	ACC	TTC	AAC	CCA	AAC	AAG	CGC	ATC	960	
	Leu	Asp	Leu	Leu	Asp	Arg	Met	Leu	Thr	Phe	Asn	Pro	Asn	Lys	Arg	Ile		
	305					310					315					320		
25	ACA	GTA	GAG	GAA	GCG	CTG	GCT	CAC	CCT	TAC	CTG	GAA	CAG	TAC	TAC	GAT	1008	
	Thr	Val	Glu	Glu	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp		
					325					330					335			
30	CCG	ACA	GAT	GAG	CCA	GTG	GCC	GAG	GAG	CCA	TTC	ACC	TTC	GAC	ATG	GAG	1056	
	Pro	Thr	Asp	Glu	Pro	Val	Ala	Glu	Glu	Pro	Phe	Thr	Phe	Asp	Met	Glu		
				340				345						350				
35	CTG	GAT	GAC	CTC	CCC	AAG	GAG	CGG	CTG	AAG	GAG	TTG	ATC	TTC	CAG	GAG	1104	
	Leu	Asp	Asp	Leu	Pro	Lys	Glu	Arg	Leu	Lys	Glu	Leu	Ile	Phe	Gln	Glu		
				355				360					365					
40	ACA	GCC	CGC	TTC	CAG	CCA	GGG	GCG	CCA	GAG	GGC	CCC	GGG	CGC	GCC	ATG	1152	
	Thr	Ala	Arg	Phe	Gln	Pro	Gly	Ala	Pro	Glu	Gly	Pro	Gly	Arg	Ala	Met		
				370			375					380						
45	AGT	AAA	GGA	GAA	GAA	CTT	TTC	ACT	GGA	GTT	GTC	CCA	ATT	CTT	GTT	GAA	1200	
	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu		
	385					390					395					400		
50	TTA	GAT	GGC	GAT	GTT	AAT	GGG	CAA	AAA	TTC	TCT	GTT	AGT	GGA	GAG	GGT	1248	
	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly		
					405					410					415			
55	GAA	GGT	GAT	GCA	ACA	TAC	GGA	AAA	CTT	ACC	CTT	AAA	TTT	ATT	TGC	ACT	1296	
	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr		
				420				425					430					
60	ACT	GGG	AAG	CTA	CCT	GTT	CCA	TGG	CCA	ACG	CTT	GTC	ACT	ACT	CTC	ACT	1344	
	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr		
				435				440					445					
65	TAT	GGT	GTT	CAA	TGC	TTT	TCT	AGA	TAC	CCA	GAT	CAT	ATG	AAA	CAG			

120

	465	470	475	480	
	ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT GAA GTC AAG				1488
	Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys				
5		485	490	495	
	TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA GGT ATT GAT				1536
	Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp				
10		500	505	510	
	TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG GAA TAC AAT TAT				1584
	Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn Tyr				
		515	520	525	
15	AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA AAG AAT GGC ATC				1632
	Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile				
		530	535	540	
	AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT GGA AGC GTT CAA				1680
20	Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln				
		545	550	555	560
	TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT GGC CCT GTC				1728
	Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val				
25		565	570	575	
	CTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT GCC CTT TCC AAA				1776
	Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys				
		580	585	590	
30	GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT GAG TTT GTA ACA				1824
	Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr				
		595	600	605	
35	GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA CCT CAG GAG T				1873
	Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Gln Glu				
		610	615	620	
40	AA				1875

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Gly	Gly	Gly	Gly	Gly	Glu	Pro	Arg
1				5				10					15		
Gly	Thr	Ala	Gly	Val	Val	Pro	Val	Val	Pro	Gly	Glu	Val	Glu	Val	Val

120

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		20		25		30											
	Lys	Gly	Gln	Pro	Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Gln	Leu	Gln	Tyr	
		35						40					45				
5	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Met	Val	Ser	Ser	Ala	Tyr	Asp	His	Val	
		50					55					60					
	Arg	Lys	Thr	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln	
	65					70				75				80			
	Thr	Tyr	Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Gln	Ile	Leu	Leu	Arg	Phe	
					85				90					95			
10	Arg	His	Glu	Asn	Val	Ile	Gly	Ile	Arg	Asp	Ile	Leu	Arg	Ala	Pro	Thr	
				100					105					110			
	Leu	Glu	Ala	Met	Arg	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	
			115					120				125					
	Asp	Leu	Tyr	Lys	Leu	Leu	Lys	Ser	Gln	Gln	Leu	Ser	Asn	Asp	His	Ile	
15		130					135				140						
	Cys	Tyr	Phe	Leu	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	
	145					150				155				160			
	Ala	Asn	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Ile	Asn	
					165				170					175			
20	Thr	Thr	Cys	Asp	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ala	
				180					185					190			
	Asp	Pro	Glu	His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	
		195					200					205					
	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	
25		210					215				220						
	Lys	Ser	Ile	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	
	225					230				235				240			
	Ser	Asn	Arg	Pro	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	
					245				250					255			
30	His	Ile	Leu	Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	
				260					265					270			
	Ile	Ile	Asn	Met	Lys	Ala	Arg	Asn	Tyr	Leu	Gln	Ser	Leu	Pro	Ser	Lys	
		275					280					285					
	Thr	Lys	Val	Ala	Trp	Ala	Lys	Leu	Phe	Pro	Lys	Ser	Asp	Ser	Lys	Ala	
35		290					295				300						
	Leu	Asp	Leu	Leu	Asp	Arg	Met	Leu	Thr	Phe	Asn	Pro	Asn	Lys	Arg	Ile	
	305					310				315				320			
	Thr	Val	Glu	Glu	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	
					325				330					335			
40	Pro	Thr	Asp	Glu	Pro	Val	Ala	Glu	Glu	Pro	Phe	Thr	Phe	Asp	Met	Glu	
				340					345					350			
	Leu	Asp	Asp	Leu	Pro	Lys	Glu	Arg	Leu	Lys	Glu	Leu	Ile	Phe	Gln	Glu	
		355					360					365					
	Thr	Ala	Arg	Phe	Gln	Pro	Gly	Ala	Pro	Glu	Gly	Pro	Gly	Arg	Ala	Met	
45		370					375				380						
	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
	385					390				395				400			
	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
				405					410					415			
50	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	
				420					425					430			
	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	
		435					440					445					
	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	
55		450					455				460						
	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	

121

122

465 470 475 480
 Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 485 490 495
 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 5 500 505 510
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn Tyr
 515 520 525
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile
 530 535 540
 10 Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln
 545 550 555 560
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 565 570 575
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
 15 580 585 590
 Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr
 595 600 605
 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Gln Glu
 610 615 620
 20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1815 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1811
 (D) OTHER INFORMATION:

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

40 ATG GCG GCG GCG GCG GCG GCG GGC CCG GAG ATG GTC CGC GGG CAG GTG 48
 Met Ala Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val
 1 5 10 15
 TTC GAC GTG GGG CCG CGC TAC ACT AAT CTC TCG TAC ATC GGA GAA GGC 96
 Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly
 20 25 30
 45 GCC TAC GGC ATG GTT TGT TCT GCT TAT GAT AAT CTC AAC AAA GTT CGA 144
 Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Leu Asn Lys Val Arg
 35 40 45
 50 GTT GCT ATC AAG AAA ATC AGT CCT TTT GAG CAC CAG ACC TAC TGT CAG 192
 Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln
 50 55 60
 AGA ACC CTG AGA GAG ATA AAA ATC CTA CTG CGC TTC AGA CAT GAG AAC 240
 55 Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His Glu Asn
 65 70 75 80

122

123

5	ATC	ATC	GGC	ATC	AAT	GAC	ATC	ATC	CGG	GCA	CCA	ACC	ATT	GAG	CAG	ATG	288
	Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg	Ala	Pro	Thr	Ile	Glu	Gln	Met	
					85					90					95		
10	AAA	GAT	GTA	TAT	ATA	GTA	CAG	GAC	CTC	ATG	GAG	ACA	GAT	CTT	TAC	AAG	336
	Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu	Tyr	Lys	
				100					105					110			
15	CTC	TTG	AAG	ACA	CAG	CAC	CTC	AGC	AAT	GAT	CAT	ATC	TGC	TAT	TTT	CTT	384
	Leu	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr	Phe	Leu	
			115					120					125				
20	TAT	CAG	ATC	CTG	AGA	GGA	TTA	AAG	TAT	ATA	CAT	TCA	GCT	AAT	GTT	CTG	432
	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn	Val	Leu	
		130					135					140					
25	CAC	CGT	GAC	CTC	AAG	CCT	TCC	AAC	CTC	CTG	CTG	AAC	ACC	ACT	TGT	GAT	480
	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Leu	Asn	Thr	Thr	Cys	Asp	
	145					150					155				160		
30	CTC	AAG	ATC	TGT	GAC	TTT	GGC	CTT	GCC	CGT	GTT	GCA	GAT	CCA	GAC	CAT	528
	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Val	Ala	Asp	Pro	Asp	His	
				165					170						175		
35	GAT	CAT	ACA	GGG	TTC	TTG	ACA	GAG	TAT	GTA	GCC	ACG	CGT	TGG	TAC	AGA	576
	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	
			180					185					190				
40	GCT	CCA	GAA	ATT	ATG	TTG	AAT	TCC	AAG	GGT	TAT	ACC	AAG	TCC	ATT	GAT	624
	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	Asp	
		195					200					205					
45	ATT	TGG	TCT	GTG	GGC	TGC	ATC	CTG	GCA	GAG	ATG	CTA	TCC	AAC	AGG	CCT	672
	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	Pro	
		210				215						220					
50	ATC	TTC	CCA	GGA	AAG	CAT	TAC	CTT	GAC	CAG	CTG	AAT	CAC	ATC	CTG	GGT	720
	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	Gly	
	225					230				235					240		
55	ATT	CTT	GGA	TCT	CCA	TCA	CAG	GAA	GAT	CTG	AAT	TGT	ATA	ATA	AAT	TTA	768
	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	Leu	
				245					250				255				
60	AAA	GCT	AGA	AAC	TAT	TTG	CTT	TCT	CTC	CCG	CAC	AAA	AAT	AAG	GTG	CCG	816
	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	Pro	His	Lys	Asn	Lys	Val	Pro	
			260					265					270				
65	TGG	AAC	AGG	TTG	TTC	CCA	AAC	GCT	GAC	TCC	AAA	GCT	CTG	GAT	TTA	CTG	864
	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	Ser	Lys	Ala	Leu	Asp	Leu	Leu	
		275					280					285					
70	GAT	AAA	ATG	TTG	ACA	TTT	AAC	CCT	CAC	AAG	AGG	ATT	GAA	GTT	GAA	CAG	912
	Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Glu	Val	Glu	Gln	
	290					295					300						

123

124

	GCT CTG GCC CAC CCG TAC CTG GAG CAG TAT TAT GAC CCA AGT GAT GAG	960
	Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser Asp Glu	
	305 310 315 320	
5	CCC ATT GCT GAA GCA CCA TTC AAG TTT GAC ATG GAG CTG GAC GAC TTA	1008
	Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp Asp Leu	
	325 330 335	
10	CCT AAG GAG AAG CTC AAA GAA CTC ATT TTT GAA GAG ACT GCT CGA TTC	1056
	Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala Arg Phe	
	340 345 350	
15	CAG CCA GGA TAC AGA TCT ATG GAT CCA CCG GTC GCC ACC ATG GTG AGC	1104
	Gln Pro Gly Tyr Arg Ser Met Asp Pro Pro Val Ala Thr Met Val Ser	
	355 360 365	
20	AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG	1152
	Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu	
	370 375 380	
25	GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG	1200
	Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu	
	385 390 395 400	
30	GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC	1296
	Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr	
	420 425 430	
35	GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC	1344
	Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp	
	435 440 445	
40	TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC	1392
	Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile	
	450 455 460	
45	TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC	1440
	Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe	
	465 470 475 480	
50	GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC	1488
	Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe	
	485 490 495	
55	AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC	1536
	Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn	
	500 505 510	
55	AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG	1584
	Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys	
	515 520 525	

124

125

GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC 1632
 Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 530 535 540

5

GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG 1680
 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 545 550 555 560

10

CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC 1728
 Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
 565 570 575

15

CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC 1776
 Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
 580 585 590

20

GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AA GTAA 1815
 Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 595 600

(2) INFORMATION FOR SEQ ID NO:59:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

35

Met Ala Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val
 1 5 10 15
 Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly
 20 25 30
 40 Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Leu Asn Lys Val Arg
 35 40 45
 Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln
 50 55 60
 Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His Glu Asn
 45 65 70 75 80
 Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu Gln Met
 85 90 95
 Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys
 100 105 110
 50 Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr Phe Leu
 115 120 125
 Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu
 130 135 140
 His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Thr Thr Cys Asp
 55 145 150 155 160
 Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro Asp His

125

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					165					170					175				
	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg			
				180						185					190				
5	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	Asp			
			195						200					205					
	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	Pro			
		210					215						220						
	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	Gly			
	225					230					235				240				
10	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	Leu			
					245					250					255				
	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	Pro	His	Lys	Asn	Lys	Val	Pro			
				260					265					270					
	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	Ser	Lys	Ala	Leu	Asp	Leu	Leu			
15			275					280					285						
	Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Glu	Val	Glu	Gln			
	290						295					300							
	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Ser	Asp	Glu			
	305					310					315				320				
20	Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe	Asp	Met	Glu	Leu	Asp	Asp	Leu			
					325					330					335				
	Pro	Lys	Glu	Lys	Leu	Lys	Glu	Leu	Ile	Phe	Glu	Glu	Thr	Ala	Arg	Phe			
				340					345					350					
	Gln	Pro	Gly	Tyr	Arg	Ser	Met	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser			
25			355					360					365						
	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu			
	370						375					380							
	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu			
	385					390					395				400				
30	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr			
					405					410					415				
	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr			
				420					425					430					
	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp			
35			435					440					445						
	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile			
		450					455					460							
	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe			
	465					470					475				480				
40	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe			
					485					490					495				
	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn			
				500					505					510					
	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys			
45			515					520					525						
	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu			
		530					535					540							
	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu			
	545					550					555				560				
50	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp			
				565						570					575				
	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala			
				580					585					590					
	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys							
55			595					600											

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(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2508
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

5	ATG GAG CTG GAA AAC ATC GTG GCC AAC ACG GTC TTG CTG AAA GCC AGG	48
10	Met Glu Leu Glu Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg	
	1 5 10 15	
20	GAA GGG GGC GGA GGA AAG CGC AAA GGG AAA AGC AAG AAG TGG AAA GAA	96
	Glu Gly Gly Gly Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu	
	20 25 30	
25	ATC CTG AAG TTC CCT CAC ATT AGC CAG TGT GAA GAC CTC CGA AGG ACC	144
	Ile Leu Lys Phe Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr	
	35 40 45	
30	ATA GAC AGA GAT TAC TGC AGT TTA TGT GAC AAG CAG CCA ATC GGG AGG	192
	Ile Asp Arg Asp Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg	
	50 55 60	
35	CTG CTT TTC CGG CAG TTT TGT GAA ACC AGG CCT GGG CTG GAG TGT TAC	240
	Leu Leu Phe Arg Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr	
	65 70 75 80	
40	ATT CAG TTC CTG GAC TCC GTG GCA GAA TAT GAA GTT ACT CCA GAT GAA	288
	Ile Gln Phe Leu Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu	
	85 90 95	
45	AAA CTG GGA GAG AAA GGG AAG GAA ATT ATG ACC AAG TAC CTC ACC CCA	336
	Lys Leu Gly Glu Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro	
	100 105 110	
50	AAG TCC CCT GTT TTC ATA GCC CAA GTT GGC CAA GAC CTG GTC TCC CAG	384
	Lys Ser Pro Val Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln	
	115 120 125	
55	ACG GAG GAG AAG CTC CTA CAG AAG CCG TGC AAA GAA CTC TTT TCT GCC	432
	Thr Glu Glu Lys Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala	
	130 135 140	
55	TGT GCA CAG TCT GTC CAC GAG TAC CTG AGG GGA GAA CCA TTC CAC GAA	480
	Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu	
	145 150 155 160	

127

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	TAT CTG GAC AGC ATG TTT TTT GAC CGC TTT CTC CAG TGG AAG TGG TTG	528
	Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu	
	165 170 175	
5	GAA AGG CAA CCG GTG ACC AAA AAC ACT TTC AGG CAG TAT CGA GTG CTA	576
	Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu	
	180 185 190	
10	GGA AAA GGG GGC TTC GGG GAG GTC TGT GCC TGC CAG GTT CGG GCC ACG	624
	Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr	
	195 200 205	
15	GGT AAA ATG TAT GCC TGC AAG CGC TTG GAG AAG AAG AGG ATC AAA AAG	672
	Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys	
	210 215 220	
20	AGG AAA GGG GAG TCC ATG GCC CTC AAT GAG AAG CAG ATC CTC GAG AAG	720
	Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys	
	225 230 235 240	
25	GTC AAC AGT CAG TTT GTG GTC AAC CTG GCC TAT GCC TAC GAG ACC AAG	768
	Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys	
	245 250 255	
30	GAT GCA CTG TGC TTG GTC CTG ACC ATC ATG AAT GGG GGT GAC CTG AAG	816
	Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys	
	260 265 270	
35	TTC CAC ATC TAC AAC ATG GGC AAC CCT GGC TTC GAG GAG GAG CGG GCC	864
	Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala	
	275 280 285	
40	TTG TTT TAT GCG GCA GAG ATC CTC TGC GGC TTA GAA GAC CTC CAC CGT	912
	Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg	
	290 295 300	
45	GAG AAC ACC GTC TAC CGA GAT CTG AAA CCT GAA AAC ATC CTG TTA GAT	960
	Glu Asn Thr Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp	
	305 310 315 320	
50	GAT TAT GGC CAC ATT AGG ATC TCA GAC CTG GGC TTG GCT GTG AAG ATC	1008
	Asp Tyr Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile	
	325 330 335	
55	CCC GAG GGA GAC CTG ATC CGC GGC CGG GTG GGC ACT GTT GGC TAC ATG	1056
	Pro Glu Gly Asp Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met	
	340 345 350	
60	GCC CCC GAA GTC CTG AAC AAC CAG AGG TAC GGC CTG AGC CCC GAC TAC	1104
	Ala Pro Glu Val Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr	
	355 360 365	
65	TGG GGC CTT GGC TGC CTC ATC TAT GAG ATG ATC GAG GGC CAG TCG CCG	1152
	Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro	
	370 375 380	

128

	TTC CGC GGC CGT AAG GAG AAG GTG AAG CGG GAG GAG GTG GAC CGC CGG	1200
	Phe Arg Gly Arg Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg	
	385 390 395 400	
5	GTC CTG GAG ACG GAG GAG GTG TAC TCC CAC AAG TTC TCC GAG GAG GCC	1248
	Val Leu Glu Thr Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala	
	405 410 415	
10	AAG TCC ATC TGC AAG ATG CTG CTC ACG AAA GAT GCG AAG CAG AGG CTG	1296
	Lys Ser Ile Cys Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu	
	420 425 430	
15	GGC TGC CAG GAG GAG GGG GCT GCA GAG GTC AAG AGA CAC CCC TTC TTC	1344
	Gly Cys Gln Glu Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe	
	435 440 445	
20	AGG AAC ATG AAC TTC AAG CGC TTA GAA GCC GGG ATG TTG GAC CCT CCC	1392
	Arg Asn Met Asn Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro	
	450 455 460	
25	TTC GTT CCA GAC CCC CGC GCT GTG TAC TGT AAG GAC GTG CTG GAC ATC	1440
	Phe Val Pro Asp Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile	
	465 470 475 480	
30	GAG CAG TTC TCC ACT GTG AAG GGC GTC AAT CTG GAC CAC ACA GAC GAC	1488
	Glu Gln Phe Ser Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp	
	485 490 495	
35	GAC TTC TAC TCC AAG TTC TCC ACG GGC TCT GTG TCC ATC CCA TGG CAA	1536
	Asp Phe Tyr Ser Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln	
	500 505 510	
40	AAC GAG ATG ATA GAA ACA GAA TGC TTT AAG GAG CTG AAC GTG TTT GGA	1584
	Asn Glu Met Ile Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly	
	515 520 525	
45	CCT AAT GGT ACC CTC CCG CCA GAT CTG AAC AGA AAC CAC CCT CCG GAA	1632
	Pro Asn Gly Thr Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu	
	530 535 540	
50	CCG CCC AAG AAA GGG CTG CTC CAG AGA CTC TTC AAG CGG CAG CAT CAG	1680
	Pro Pro Lys Lys Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln	
	545 550 555 560	
55	AAC AAT TCC AAG AGT TCG CCC AGC TCC AAG ACC AGT TTT AAC CAC CAC	1728
	Asn Asn Ser Lys Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His	
	565 570 575	
60	ATA AAC TCA AAC CAT GTC AGC TCG AAC TCC ACC GGA AGC AGC AGG GAT	1776
	Ile Asn Ser Asn His Val Ser Ser Asn Ser Thr Gly Ser Ser Arg Asp	
	580 585 590	
65	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG	1824
	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly	
	595 600 605	

130

	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	1872
	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	
	610						615					620					
5	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	1920
	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	
	625					630				635						640	
10	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	1968
	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	
					645					650						655	
15	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	2016
	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	
				660					665						670		
20	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	2064
	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	
			675					680						685			
25	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	2112
	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	
	690					695						700					
30	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	2160
	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	
	705				710						715					720	
35	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	2208
	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	
					725					730					735		
40	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	2256
	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	
				740					745					750			
45	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	2304
	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	
			755					760						765			
50	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	2352
	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	
	770						775					780					
55	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	2400
	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	
	785					790					795					800	
60	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	2448
	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	
					805					810						815	
65	GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	2496
	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	
				820					825					830			

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GAG CTG TAC AAG TAA
 Glu Leu Tyr Lys
 835

2511

5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 836 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

20 Met Glu Leu Glu Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg
 1 5 10 15
 Glu Gly Gly Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu
 20 25 30
 Ile Leu Lys Phe Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr
 35 40 45
 25 Ile Asp Arg Asp Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
 50 55 60
 Leu Leu Phe Arg Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr
 65 70 75 80
 30 Ile Gln Phe Leu Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu
 85 90 95
 Lys Leu Gly Glu Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro
 100 105 110
 Lys Ser Pro Val Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln
 115 120 125
 35 Thr Glu Glu Lys Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala
 130 135 140
 Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu
 145 150 155 160
 40 Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu
 165 170 175
 Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu
 180 185 190
 Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr
 195 200 205
 45 Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys
 210 215 220
 Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys
 225 230 235 240
 50 Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys
 245 250 255
 Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys
 260 265 270
 Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala
 275 280 285
 55 Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg

131

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	290		295		300														
	Glu	Asn	Thr	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp			
	305					310					315					320			
5	Asp	Tyr	Gly	His	Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Val	Lys	Ile			
					325					330						335			
	Pro	Glu	Gly	Asp	Leu	Ile	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr	Met			
				340					345							350			
	Ala	Pro	Glu	Val	Leu	Asn	Asn	Gln	Arg	Tyr	Gly	Leu	Ser	Pro	Asp	Tyr			
				355				360								365			
10	Trp	Gly	Leu	Gly	Cys	Leu	Ile	Tyr	Glu	Met	Ile	Glu	Gly	Gln	Ser	Pro			
	370						375					380							
	Phe	Arg	Gly	Arg	Lys	Glu	Lys	Val	Lys	Arg	Glu	Glu	Val	Asp	Arg	Arg			
	385					390					395					400			
	Val	Leu	Glu	Thr	Glu	Glu	Val	Tyr	Ser	His	Lys	Phe	Ser	Glu	Glu	Ala			
15					405					410						415			
	Lys	Ser	Ile	Cys	Lys	Met	Leu	Leu	Thr	Lys	Asp	Ala	Lys	Gln	Arg	Leu			
				420					425							430			
	Gly	Cys	Gln	Glu	Glu	Gly	Ala	Ala	Glu	Val	Lys	Arg	His	Pro	Phe	Phe			
				435			440						445						
20	Arg	Asn	Met	Asn	Phe	Lys	Arg	Leu	Glu	Ala	Gly	Met	Leu	Asp	Pro	Pro			
	450						455					460							
	Phe	Val	Pro	Asp	Pro	Arg	Ala	Val	Tyr	Cys	Lys	Asp	Val	Leu	Asp	Ile			
	465					470					475					480			
	Glu	Gln	Phe	Ser	Thr	Val	Lys	Gly	Val	Asn	Leu	Asp	His	Thr	Asp	Asp			
25					485				490							495			
	Asp	Phe	Tyr	Ser	Lys	Phe	Ser	Thr	Gly	Ser	Val	Ser	Ile	Pro	Trp	Gln			
				500					505						510				
	Asn	Glu	Met	Ile	Glu	Thr	Glu	Cys	Phe	Lys	Glu	Leu	Asn	Val	Phe	Gly			
				515			520						525						
30	Pro	Asn	Gly	Thr	Leu	Pro	Pro	Asp	Leu	Asn	Arg	Asn	His	Pro	Pro	Glu			
	530						535					540							
	Pro	Pro	Lys	Lys	Gly	Leu	Leu	Gln	Arg	Leu	Phe	Lys	Arg	Gln	His	Gln			
	545					550					555					560			
	Asn	Asn	Ser	Lys	Ser	Ser	Pro	Ser	Ser	Lys	Thr	Ser	Phe	Asn	His	His			
35					565				570							575			
	Ile	Asn	Ser	Asn	His	Val	Ser	Ser	Asn	Ser	Thr	Gly	Ser	Ser	Arg	Asp			
				580					585						590				
	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly			
				595				600						605					
40	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys			
	610						615					620							
	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu			
	625					630					635					640			
	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro			
45					645					650						655			
	Thr	Leu	Val	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr				
				660				665							670				
	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu			
				675				680					685						
50	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr			
	690						695					700							
	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg			
	705					710					715					720			
	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly			
55					725					730						735			
	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala			

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740 745 750
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
 755 760 765
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 5 770 775 780
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 785 790 795 800
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 805 810 815
 10 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 820 825 830
 Glu Leu Tyr Lys
 835

15 (2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1893 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 25 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1890
 (D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATG AGC AGA AGC AAG CGT GAC AAC AAT TTT TAT AGT GTA GAG ATT GGA 48
 Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly
 1 5 10 15
 35 GAT TCT ACA TTC ACA GTC CTG AAA CGA TAT CAG AAT TTA AAA CCT ATA 96
 Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile
 20 25 30
 40 GGC TCA GGA GCT CAA GGA ATA GTA TGC GCA GCT TAT GAT GCC ATT CTT 144
 Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu
 35 40 45
 45 GAA AGA AAT GTT GCA ATC AAG AAG CTA AGC CGA CCA TTT CAG AAT CAG 192
 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
 50 55 60
 ACT CAT GCC AAG CGG GCC TAC AGA GAG CTA GTT CTT ATG AAA TGT GTT 240
 Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val
 50 65 70 75 80
 AAT CAC AAA AAT ATA ATT GGC CTT TTG AAT GTT TTC ACA CCA CAG AAA 288
 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys
 85 90 95
 55 TCC CTA GAA GAA TTT CAA GAT GTT TAC ATA GTC ATG GAG CTC ATG GAT 336

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	Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp	
				100					105					110			
5	GCA	AAT	CTT	TGC	CAA	GTG	ATT	CAG	ATG	GAG	CTA	GAT	CAT	GAA	AGA	ATG	384
	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met	
			115					120					125				
10	TCC	TAC	CTT	CTC	TAT	CAG	ATG	CTG	TGT	GGA	ATC	AAG	CAC	CTT	CAT	TCT	432
	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	
			130				135					140					
15	GCT	GGA	ATT	ATT	CAT	CGG	GAC	TTA	AAG	CCC	AGT	AAT	ATA	GTA	GTA	AAA	480
	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	
	145					150				155						160	
	TCT	GAT	TGC	ACT	TTG	AAG	ATT	CTT	GAC	TTC	GGT	CTG	GCC	AGG	ACT	GCA	528
	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
				165						170					175		
20	GGA	ACG	AGT	TTT	ATG	ATG	ACG	CCT	TAT	GTA	GTG	ACT	CGC	TAC	TAC	AGA	576
	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
				180					185					190			
25	GCA	CCC	GAG	GTC	ATC	CTT	GGC	ATG	GGC	TAC	AAG	GAA	AAC	GTG	GAT	TTA	624
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu	
			195					200					205				
30	TGG	TCT	GTG	GGG	TGC	ATT	ATG	GGA	GAA	ATG	GTT	TGC	CAC	AAA	ATC	CTC	672
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu	
		210					215					220					
35	TTT	CCA	GGA	AGG	GAC	TAT	ATT	GAT	CAG	TGG	AAT	AAA	GTT	ATT	GAA	CAG	720
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
	225					230					235					240	
	CTT	GGA	ACA	CCA	TGT	CCT	GAA	TTC	ATG	AAG	AAA	CTG	CAA	CCA	ACA	GTA	768
	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
				245						250					255		
40	AGG	ACT	TAC	GTT	GAA	AAC	AGA	CCT	AAA	TAT	GCT	GGA	TAT	AGC	TTT	GAG	816
	Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu	
				260					265					270			
45	AAA	CTC	TTC	CCT	GAT	GTC	CTT	TTC	CCA	GCT	GAC	TCA	GAA	CAC	AAC	AAA	864
	Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys	
			275					280					285				
50	CTT	AAA	GCC	AGT	CAG	GCA	AGG	GAT	TTG	TTA	TCC	AAA	ATG	CTG	GTA	ATA	912
	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
			290				295					300					
55	GAT	GCA	TCT	AAA	AGG	ATC	TCT	GTA	GAT	GAA	GCT	CTC	CAA	CAC	CCG	TAC	960
	Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr	
	305					310					315					320	
	ATC	AAT	GTC	TGG	TAT	GAT	CCT	TCT	GAA	GCA	GAA	GCT	CCA	CCA	CCA	AAG	1008

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	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys	
					325					330					335		
5	ATC	CCT	GAC	AAG	CAG	TTA	GAT	GAA	AGG	GAA	CAC	ACA	ATA	GAA	GAG	TGG	1056
	Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp	
				340					345					350			
10	AAA	GAA	TTG	ATA	TAT	AAG	GAA	GTT	ATG	GAC	TTG	GAG	GAG	AGA	ACC	AAG	1104
	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys	
			355					360					365				
15	AAT	GGA	GTT	ATA	CGG	GGG	CAG	CCC	TCT	CCT	TTA	GCA	CAG	GTG	CAG	CAG	1152
	Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln	
		370					375					380					
20	TGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	1200
	Trp	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	
	385					390				395					400		
25	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	1248
	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	
					405				410						415		
30	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	1296
	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	
				420					425					430			
35	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	1344
	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	
			435				440						445				
40	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	1392
	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	
		450				455					460						
45	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	1440
	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	
	465				470					475					480		
50	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	1488
	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	
					485				490					495			
55	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	1536
	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	
				500					505					510			
60	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	1584
	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	
			515					520					525				
65	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	1632
	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	
		530					535					540					
70	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	1680

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Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 545 550 555 560

5 CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG 1728
 His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
 565 570 575

10 AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC 1776
 Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
 580 585 590

CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT 1824
 Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 595 600 605

15 CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC 1872
 His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly
 610 615 620

20 ATG GAC GAG CTG TAC AAG TAA 1893
 Met Asp Glu Leu Tyr Lys
 625 630

25 (2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly
 1 5 10 15
 40 Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile
 20 25 30
 Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu
 35 40 45
 45 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
 50 55 60
 Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val
 65 70 75 80
 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys
 85 90 95
 50 Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp
 100 105 110
 Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met
 115 120 125
 Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser
 130 135 140
 55 Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys

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	145				150				155				160			
	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala
					165					170					175	
	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg
5				180					185					190		
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu
			195					200					205			
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu
		210					215					220				
10	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln
	225					230					235				240	
	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val
				245						250					255	
	Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu
15				260					265					270		
	Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys
			275					280					285			
	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile
		290					295					300				
20	Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr
	305					310					315				320	
	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys
				325						330					335	
	Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp
25				340					345					350		
	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys
			355					360					365			
	Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln
		370					375					380				
30	Trp	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe
	385					390					395				400	
	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly
				405						410					415	
	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly
35				420					425					430		
	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro
			435					440					445			
	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser
		450					455					460				
40	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met
	465					470					475				480	
	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly
				485						490					495	
	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val
45				500					505					510		
	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile
			515					520					525			
	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile
		530					535					540				
50	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg
	545					550					555				560	
	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln
				565						570					575	
	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr
55				580					585					590		
	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp

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[illegible]

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1821 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

- 20 (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1818
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

25	ATG	TCT	CAG	GAG	AGG	CCC	ACG	TTC	TAC	CGG	CAG	GAG	CTG	AAC	AAG	ACA	48
	Met	Ser	Gln	Glu	Arg	Pro	Thr	Phe	Tyr	Arg	Gln	Glu	Leu	Asn	Lys	Thr	
	1				5					10					15		
30	ATC	TGG	GAG	GTG	CCC	GAG	CGT	TAC	CAG	AAC	CTG	TCT	CCA	GTG	GGC	TCT	96
	Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln	Asn	Leu	Ser	Pro	Val	Gly	Ser	
				20				25						30			
35	GGC	GCC	TAT	GGC	TCT	GTG	TGT	GCT	GCT	TTT	GAC	ACA	AAA	ACG	GGG	TTA	144
	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala	Phe	Asp	Thr	Lys	Thr	Gly	Leu	
			35				40						45				
40	CGT	GTG	GCA	GTG	AAG	AAG	CTC	TCC	AGA	CCA	TTT	CAG	TCC	ATC	ATT	CAT	192
	Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Ile	Ile	His	
		50					55					60					
45	GCG	AAA	AGA	ACC	TAC	AGA	GAA	CTG	CGG	TTA	CTT	AAA	CAT	ATG	AAA	CAT	240
	Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Met	Lys	His	
	65					70				75					80		
50	GAA	AAT	GTG	ATT	GGT	CTG	TTG	GAC	GTT	TTT	ACA	CCT	GCA	AGG	TCT	CTG	288
	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Arg	Ser	Leu	
					85				90						95		
55	GAG	GAA	TTC	AAT	GAT	GTG	TAT	CTG	GTG	ACC	CAT	CTC	ATG	GGG	GCA	GAT	336
	Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val	Thr	His	Leu	Met	Gly	Ala	Asp	
				100				105						110			
60	CTG	AAC	AAC	ATT	GTG	AAA	TGT	CAG	AAG	CTT	ACA	GAT	GAC	CAT	GTT	CAG	384
	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys	Leu	Thr	Asp	Asp	His	Val	Gln	
			115				120						125				
65	TTC	CTT	ATC	TAC	CAA	ATT	CTC	CGA	GGT	CTA	AAG	TAT	ATA	CAT	TCA	GCT	432

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	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	
	130						135					140					
5	GAC	ATA	ATT	CAC	AGG	GAC	CTA	AAA	CCT	AGT	AAT	CTA	GCT	GTG	AAT	GAA	480
	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Ala	Val	Asn	Glu	
	145					150					155					160	
10	GAC	TGT	GAG	CTG	AAG	ATT	CTG	GAT	TTT	GGA	CTG	GCT	CGG	CAC	ACA	GAT	528
	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Thr	Asp	
				165					170						175		
15	GAT	GAA	ATG	ACA	GGC	TAC	GTG	GCC	ACT	AGG	TGG	TAC	AGG	GCT	CCT	GAG	576
	Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	
				180					185					190			
20	ATC	ATG	CTG	AAC	TGG	ATG	CAT	TAC	AAC	CAG	ACA	GTT	GAT	ATT	TGG	TCA	624
	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	
		195					200						205				
25	GTG	GGA	TGC	ATA	ATG	GCC	GAG	CTG	TTG	ACT	GGA	AGA	ACA	TTG	TTT	CCT	672
	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Thr	Gly	Arg	Thr	Leu	Phe	Pro	
		210					215					220					
30	GGT	ACA	GAC	CAT	ATT	GAT	CAG	TTG	AAG	CTC	ATT	TTA	AGA	CTC	GTT	GGA	720
	Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys	Leu	Ile	Leu	Arg	Leu	Val	Gly	
	225					230					235					240	
35	ACC	CCA	GGG	GCT	GAG	CTT	TTG	AAG	AAA	ATC	TCC	TCA	GAG	TCT	GCA	AGA	768
	Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys	Ile	Ser	Ser	Glu	Ser	Ala	Arg	
				245						250					255		
40	AAC	TAT	ATT	CAG	TCT	TTG	ACT	CAG	ATG	CCG	AAG	ATG	AAC	TTT	GCG	AAT	816
	Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met	Pro	Lys	Met	Asn	Phe	Ala	Asn	
				260					265					270			
45	GTA	TTT	ATT	GGT	GCC	AAT	CCC	CTG	GCT	GTC	GAC	TTG	CTG	GAG	AAG	ATG	864
	Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala	Val	Asp	Leu	Leu	Glu	Lys	Met	
		275						280					285				
50	CTT	GTA	TTG	GAC	TCA	GAT	AAG	AGA	ATT	ACA	GCG	GCC	CAA	GCC	CTT	GCA	912
	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln	Ala	Leu	Ala	
		290					295					300					
55	CAT	GCC	TAC	TTT	GCT	CAG	TAC	CAC	GAT	CCT	GAT	GAT	GAA	CCA	GTG	GCC	960
	His	Ala	Tyr	Phe	Ala	Gln	Tyr	His	Asp	Pro	Asp	Asp	Glu	Pro	Val	Ala	
	305					310					315					320	
60	GAT	CCT	TAT	GAT	CAG	TCC	TTT	GAA	AGC	AGG	GAC	CTC	CTT	ATA	GAT	GAG	1008
	Asp	Pro	Tyr	Asp	Gln	Ser	Phe	Glu	Ser	Arg	Asp	Leu	Leu	Ile	Asp	Glu	
					325					330					335		
65	TGG	AAA	AGC	CTG	ACC	TAT	GAT	GAA	GTC	ATC	AGC	TTT	GTG	CCA	CCA	CCC	1056
	Trp	Lys	Ser	Leu	Thr	Tyr	Asp	Glu	Val	Ile	Ser	Phe	Val	Pro	Pro	Pro	
				340					345					350			
70	CTT	GAC	CAA	GAA	GAG	ATG	GAG	TCC	GAG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	1104

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	Leu	Asp	Gln	Glu	Glu	Met	Glu	Ser	Glu	Asp	Pro	Pro	Val	Ala	Thr	Met	
			355					360					365				
5	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	1152
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
			370				375					380					
10	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	1200
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			385				390				395					400	
15	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	1248
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
					405					410					415		
	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	1296
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
				420					425				430				
20	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	1344
	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
			435					440				445					
25	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	1392
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
		450					455					460					
30	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	1440
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
		465				470					475				480		
35	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	1488
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
				485					490				495				
	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	1536
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
				500					505				510				
40	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	1584
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
			515					520					525				
45	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	1632
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
		530					535					540					
50	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	1680
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
		545				550					555					560	
55	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	1728
	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
				565					570					575			
	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG	1776

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Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 580 585 590

ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 1821
 5 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 595 600 605

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
 1 5 10 15
 Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
 25 20 25 30
 Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly Leu
 35 40 45
 Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
 50 55 60
 30 Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
 65 70 75 80
 Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
 85 90 95
 Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp
 35 100 105 110
 Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
 115 120 125
 Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
 130 135 140
 40 Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
 145 150 155 160
 Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
 165 170 175
 Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
 45 180 185 190
 Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
 195 200 205
 Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
 210 215 220
 50 Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly
 225 230 235 240
 Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg
 245 250 255
 Asn Tyr Ile Gln Ser Leu Thr Gln Met Pro Lys Met Asn Phe Ala Asn
 55 260 265 270
 Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met

141

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	275					280					285					
	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln	Ala	Leu	Ala
	290						295					300				
5	His	Ala	Tyr	Phe	Ala	Gln	Tyr	His	Asp	Pro	Asp	Asp	Glu	Pro	Val	Ala
	305					310					315					320
	Asp	Pro	Tyr	Asp	Gln	Ser	Phe	Glu	Ser	Arg	Asp	Leu	Leu	Ile	Asp	Glu
					325					330					335	
	Trp	Lys	Ser	Leu	Thr	Tyr	Asp	Glu	Val	Ile	Ser	Phe	Val	Pro	Pro	Pro
				340					345					350		
10	Leu	Asp	Gln	Glu	Glu	Met	Glu	Ser	Glu	Asp	Pro	Pro	Val	Ala	Thr	Met
			355					360					365			
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
	370						375					380				
15	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
	385					390					395					400
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
					405					410					415	
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
				420					425					430		
20	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
			435					440					445			
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
	450						455					460				
25	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
	465					470					475				480	
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
					485				490						495	
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
				500				505						510		
30	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
			515					520					525			
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
	530						535					540				
35	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
	545					550					555					560
	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
					565					570					575	
	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
				580				585						590		
40	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
			595					600					605			

(2) INFORMATION FOR SEQ ID NO:66:

```

45      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2913 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

50      (ii) MOLECULE TYPE: cDNA
          (ix) FEATURE:

          (A) NAME/KEY: Coding Sequence
          (B) LOCATION: 1...2910
          (D) OTHER INFORMATION:

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

5	ATG AGT GCT GAG GGG TAC CAG TAC AGA GCG CTG TAT GAT TAT AAA AAG	48
	Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys	
	1 5 10 15	
10	GAA AGA GAA GAA GAT ATT GAC TTG CAC TTG GGT GAC ATA TTG ACT GTG	96
	Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val	
	20 25 30	
15	AAT AAA GGG TCC TTA GTA GCT CTT GGA TTC AGT GAT GGA CAG GAA GCC	144
	Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala	
	35 40 45	
20	AGG CCT GAA GAA ATT GGC TGG TTA AAT GGC TAT AAT GAA ACC ACA GGG	192
	Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly	
	50 55 60	
25	GAA AGG GGG GAC TTT CCG GGA ACT TAC GTA GAA TAT ATT GGA AGG AAA	240
	Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys	
	65 70 75 80	
30	AAA ATC TCG CCT CCC ACA CCA AAG CCC CGG CCA CCT CGG CCT CTT CCT	288
	Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro	
	85 90 95	
35	GTT GCA CCA GGT TCT TCG AAA ACT GAA GCA GAT GTT GAA CAA CAA GCT	336
	Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala	
	100 105 110	
40	TTG ACT CTC CCG GAT CTT GCA GAG CAG TTT GCC CCT CCT GAC ATT GCC	384
	Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala	
	115 120 125	
45	CCG CCT CTT CTT ATC AAG CTC GTG GAA GCC ATT GAA AAG AAA GGT CTG	432
	Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu	
	130 135 140	
50	GAA TGT TCA ACT CTA TAC AGA ACA CAG AGC TCC AGC AAC CTG GCA GAA	480
	Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser Asn Leu Ala Glu	
	145 150 155 160	
55	TTA CGA CAG CTT CTT GAT TGT GAT ACA CCC TCC GTG GAC TTG GAA ATG	528
	Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met	
	165 170 175	
60	ATC GAT GTG CAC GTT TTG GCT GAC GCT TTC AAA CGC TAT CTC CTG GAC	576
	Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp	
	180 185 190	
65	TTA CCA AAT CCT GTC ATT CCA GCA GCC GTT TAC AGT GAA ATG ATT TCT	624
	Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser	
	195 200 205	
70	TTA GCT CCA GAA GTA CAA AGC TCC GAA GAA TAT ATT CAG CTA TTG AAG	672

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	Leu	Ala	Pro	Glu	Val	Gln	Ser	Ser	Glu	Glu	Tyr	Ile	Gln	Leu	Leu	Lys	
	210						215					220					
5	AAG	CTT	ATT	AGG	TCG	CCT	AGC	ATA	CCT	CAT	CAG	TAT	TGG	CTT	ACG	CTT	720
	Lys	Leu	Ile	Arg	Ser	Pro	Ser	Ile	Pro	His	Gln	Tyr	Trp	Leu	Thr	Leu	
	225					230					235					240	
10	CAG	TAT	TTG	TTA	AAA	CAT	TTC	TTC	AAG	CTC	TCT	CAA	ACC	TCC	AGC	AAA	768
	Gln	Tyr	Leu	Leu	Lys	His	Phe	Phe	Lys	Leu	Ser	Gln	Thr	Ser	Ser	Lys	
					245					250					255		
15	AAT	CTG	TTG	AAT	GCA	AGA	GTA	CTC	TCT	GAA	ATT	TTC	AGC	CCT	ATG	CTT	816
	Asn	Leu	Leu	Asn	Ala	Arg	Val	Leu	Ser	Glu	Ile	Phe	Ser	Pro	Met	Leu	
				260					265					270			
20	TTC	AGA	TTC	TCA	GCA	GCC	AGC	TCT	GAT	AAT	ACT	GAA	AAC	CTC	ATA	AAA	864
	Phe	Arg	Phe	Ser	Ala	Ala	Ser	Ser	Asp	Asn	Thr	Glu	Asn	Leu	Ile	Lys	
		275						280					285				
25	GTT	ATA	GAA	ATT	TTA	ATC	TCA	ACT	GAA	TGG	AAT	GAA	CGA	CAG	CCT	GCA	912
	Val	Ile	Glu	Ile	Leu	Ile	Ser	Thr	Glu	Trp	Asn	Glu	Arg	Gln	Pro	Ala	
	290						295					300					
30	CCA	GCA	CTG	CCT	CCT	AAA	CCA	CCA	AAA	CCT	ACT	ACT	GTA	GCC	AAC	AAC	960
	Pro	Ala	Leu	Pro	Pro	Lys	Pro	Pro	Lys	Pro	Thr	Thr	Val	Ala	Asn	Asn	
	305					310					315				320		
35	GGT	ATG	AAT	AAC	AAT	ATG	TCC	TTA	CAA	AAT	GCT	GAA	TGG	TAC	TGG	GGA	1008
	Gly	Met	Asn	Asn	Asn	Met	Ser	Leu	Gln	Asn	Ala	Glu	Trp	Tyr	Trp	Gly	
					325					330					335		
40	GAT	ATC	TCG	AGG	GAA	GAA	GTG	AAT	GAA	AAA	CTT	CGA	GAT	ACA	GCA	GAC	1056
	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu	Lys	Leu	Arg	Asp	Thr	Ala	Asp	
				340					345					350			
45	GGG	ACC	TTT	TTG	GTA	CGA	GAT	GCG	TCT	ACT	AAA	ATG	CAT	GGT	GAT	TAT	1104
	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala	Ser	Thr	Lys	Met	His	Gly	Asp	Tyr	
		355						360					365				
50	ACT	CTT	ACA	CTA	AGG	AAA	GGG	GGA	AAT	AAC	AAA	TTA	ATC	AAA	ATA	TTT	1152
	Thr	Leu	Thr	Leu	Arg	Lys	Gly	Gly	Asn	Asn	Lys	Leu	Ile	Lys	Ile	Phe	
	370						375					380					
55	CAT	CGA	GAT	GGG	AAA	TAT	GGC	TTC	TCT	GAC	CCA	TTA	ACC	TTC	AGT	TCT	1200
	His	Arg	Asp	Gly	Lys	Tyr	Gly	Phe	Ser	Asp	Pro	Leu	Thr	Phe	Ser	Ser	
	385					390					395				400		
50	GTG	GTT	GAA	TTA	ATA	AAC	CAC	TAC	CGG	AAT	GAA	TCT	CTA	GCT	CAG	TAT	1248
	Val	Val	Glu	Leu	Ile	Asn	His	Tyr	Arg	Asn	Glu	Ser	Leu	Ala	Gln	Tyr	
					405					410					415		
55	AAT	CCC	AAA	TTG	GAT	GTG	AAA	TTA	CTT	TAT	CCA	GTA	TCC	AAA	TAC	CAA	1296
	Asn	Pro	Lys	Leu	Asp	Val	Lys	Leu	Leu	Tyr	Pro	Val	Ser	Lys	Tyr	Gln	
				420					425					430			
55	CAG	GAT	CAA	GTT	GTC	AAA	GAA	GAT	AAT	ATT	GAA	GCT	GTA	GGG	AAA	AAA	1344

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	Gln	Asp	Gln	Val	Val	Lys	Glu	Asp	Asn	Ile	Glu	Ala	Val	Gly	Lys	Lys	
			435					440					445				
5	TTA	CAT	GAA	TAT	AAC	ACT	CAG	TTT	CAA	GAA	AAA	AGT	CGA	GAA	TAT	GAT	1392
	Leu	His	Glu	Tyr	Asn	Thr	Gln	Phe	Gln	Glu	Lys	Ser	Arg	Glu	Tyr	Asp	
			450				455				460						
10	AGA	TTA	TAT	GAA	GAA	TAT	ACC	CGC	ACA	TCC	CAG	GAA	ATC	CAA	ATG	AAA	1440
	Arg	Leu	Tyr	Glu	Glu	Tyr	Thr	Arg	Thr	Ser	Gln	Glu	Ile	Gln	Met	Lys	
			465			470				475						480	
15	AGG	ACA	GCT	ATT	GAA	GCA	TTT	AAT	GAA	ACC	ATA	AAA	ATA	TTT	GAA	GAA	1488
	Arg	Thr	Ala	Ile	Glu	Ala	Phe	Asn	Glu	Thr	Ile	Lys	Ile	Phe	Glu	Glu	
				485					490						495		
20	CAG	TGC	CAG	ACC	CAA	GAG	CGG	TAC	AGC	AAA	GAA	TAC	ATA	GAA	AAG	TTT	1536
	Gln	Cys	Gln	Thr	Gln	Glu	Arg	Tyr	Ser	Lys	Glu	Tyr	Ile	Glu	Lys	Phe	
				500					505					510			
25	AAA	CGT	GAA	GGC	AAT	GAG	AAA	GAA	ATA	CAA	AGG	ATT	ATG	CAT	AAT	TAT	1584
	Lys	Arg	Glu	Gly	Asn	Glu	Lys	Glu	Ile	Gln	Arg	Ile	Met	His	Asn	Tyr	
			515				520						525				
30	GAT	AAG	TTG	AAG	TCT	CGA	ATC	AGT	GAA	ATT	ATT	GAC	AGT	AGA	AGA	AGA	1632
	Asp	Lys	Leu	Lys	Ser	Arg	Ile	Ser	Glu	Ile	Ile	Asp	Ser	Arg	Arg	Arg	
			530				535					540					
35	TTG	GAA	GAA	GAC	TTG	AAG	AAG	CAG	GCA	GCT	GAG	TAT	CGA	GAA	ATT	GAC	1680
	Leu	Glu	Glu	Asp	Leu	Lys	Lys	Gln	Ala	Ala	Glu	Tyr	Arg	Glu	Ile	Asp	
			545			550					555				560		
40	AAA	CGT	ATG	AAC	AGC	ATT	AAA	CCA	GAC	CTT	ATC	CAG	CTG	AGA	AAG	ACG	1728
	Lys	Arg	Met	Asn	Ser	Ile	Lys	Pro	Asp	Leu	Ile	Gln	Leu	Arg	Lys	Thr	
				565					570						575		
45	AGA	GAC	CAA	TAC	TTG	ATG	TGG	TTG	ACT	CAA	AAA	GGT	GTT	CGG	CAA	AAG	1776
	Arg	Asp	Gln	Tyr	Leu	Met	Trp	Leu	Thr	Gln	Lys	Gly	Val	Arg	Gln	Lys	
				580					585					590			
50	AAG	TTG	AAC	GAG	TGG	TTG	GGC	AAT	GAA	AAC	ACT	GAA	GAC	CAA	TAT	TCA	1824
	Lys	Leu	Asn	Glu	Trp	Leu	Gly	Asn	Glu	Asn	Thr	Glu	Asp	Gln	Tyr	Ser	
			595				600					605					
55	CTG	GTG	GAA	GAT	GAT	GAA	GAT	TTG	CCC	CAT	CAT	GAT	GAG	AAG	ACA	TGG	1872
	Leu	Val	Glu	Asp	Asp	Glu	Asp	Leu	Pro	His	His	Asp	Glu	Lys	Thr	Trp	
			610				615					620					
60	AAT	GTT	GGA	AGC	AGC	AAC	CGA	AAC	AAA	GCT	GAA	AAC	CTG	TTG	CGA	GGG	1920
	Asn	Val	Gly	Ser	Ser	Asn	Arg	Asn	Lys	Ala	Glu	Asn	Leu	Leu	Arg	Gly	
			625			630					635				640		
65	AAG	CGA	GAT	GGC	ACT	TTT	CTT	GTC	CGG	GAG	AGC	AGT	AAA	CAG	GGC	TGC	1968
	Lys	Arg	Asp	Gly	Thr	Phe	Leu	Val	Arg	Glu	Ser	Ser	Lys	Gln	Gly	Cys	
				645					650						655		
70	TAT	GCC	TGC	TCT	GTA	GTG	GTG	GAC	GGC	GAA	GTA	AAG	CAT	TGT	GTC	ATA	2016

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	Tyr	Ala	Cys	Ser	Val	Val	Val	Asp	Gly	Glu	Val	Lys	His	Cys	Val	Ile	
				660					665					670			
5	AAC	AAA	ACA	GCA	ACT	GGC	TAT	GGC	TTT	GCC	GAG	CCC	TAT	AAC	TTG	TAC	2064
	Asn	Lys	Thr	Ala	Thr	Gly	Tyr	Gly	Phe	Ala	Glu	Pro	Tyr	Asn	Leu	Tyr	
				675				680					685				
10	AGC	TCT	CTG	AAA	GAA	CTG	GTG	CTA	CAT	TAC	CAA	CAC	ACC	TCC	CTT	GTG	2112
	Ser	Ser	Leu	Lys	Glu	Leu	Val	Leu	His	Tyr	Gln	His	Thr	Ser	Leu	Val	
				690				695					700				
15	CAG	CAC	AAC	GAC	TCC	CTC	AAT	GTC	ACA	CTA	GCC	TAC	CCA	GTA	TAT	GCA	2160
	Gln	His	Asn	Asp	Ser	Leu	Asn	Val	Thr	Leu	Ala	Tyr	Pro	Val	Tyr	Ala	
	705					710					715				720		
	CAG	CAG	AGG	CGA	CAG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	2208
	Gln	Gln	Arg	Arg	Gln	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	
					725					730					735		
20	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	2256
	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	
				740					745					750			
25	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	2304
	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	
			755					760					765				
30	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	2352
	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	
		770					775					780					
35	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	2400
	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	
	785					790					795				800		
	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	2448
	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	
					805					810					815		
40	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	2496
	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	
				820					825					830			
45	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	2544
	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	
			835					840					845				
50	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	2592
	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	
		850					855					860					
55	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	2640
	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	
	865					870					875				880		
	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	2688

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Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
885 890 895

5 TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC 2736
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
900 905 910

10 CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC 2784
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
915 920 925

GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC 2832
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
930 935 940

15 GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG 2880
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
945 950 955 960

20 ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 2913
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
965 970

25 (2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys
1 5 10 15

40 Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val
20 25 30

Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala
35 40 45

Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly
50 55 60

Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys
65 70 75 80

Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro
85 90 95

50 Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Glu Ala
100 105 110

Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala
115 120 125

Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu
130 135 140

55 Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser Asn Leu Ala Glu

147

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	145		150		155		160
	Leu	Arg	Gln	Leu	Leu	Asp	Cys
				165		170	
	Ile	Asp	Val	His	Val	Leu	Ala
5			180			185	
	Leu	Pro	Asn	Pro	Val	Ile	Pro
			195			200	
	Leu	Ala	Pro	Glu	Val	Gln	Ser
			210			215	
10	Lys	Leu	Ile	Arg	Ser	Pro	Ser
			225			230	
	Gln	Tyr	Leu	Leu	Lys	His	Phe
					245		250
	Asn	Leu	Leu	Asn	Ala	Arg	Val
15			260			265	
	Phe	Arg	Phe	Ser	Ala	Ala	Ser
			275			280	
	Val	Ile	Glu	Ile	Leu	Ile	Ser
			290			295	
20	Pro	Ala	Leu	Pro	Pro	Lys	Pro
			305			310	
	Gly	Met	Asn	Asn	Asn	Met	Ser
					325		330
	Asp	Ile	Ser	Arg	Glu	Glu	Val
25			340			345	
	Gly	Thr	Phe	Leu	Val	Arg	Asp
			355			360	
	Thr	Leu	Thr	Leu	Arg	Lys	Gly
			370			375	
30	His	Arg	Asp	Gly	Lys	Tyr	Gly
			385			390	
	Val	Val	Glu	Leu	Ile	Asn	His
					405		410
	Asn	Pro	Lys	Leu	Asp	Val	Lys
35			420			425	
	Gln	Asp	Gln	Val	Val	Lys	Glu
			435			440	
	Leu	His	Glu	Tyr	Asn	Thr	Gln
			450			455	
40	Arg	Leu	Tyr	Glu	Glu	Tyr	Thr
			465			470	
	Arg	Thr	Ala	Ile	Glu	Ala	Phe
					485		490
	Gln	Cys	Gln	Thr	Gln	Glu	Arg
45			500			505	
	Lys	Arg	Glu	Gly	Asn	Glu	Lys
			515			520	
	Asp	Lys	Leu	Lys	Ser	Arg	Ile
			530			535	
50	Leu	Glu	Glu	Asp	Leu	Lys	Gln
			545			550	
	Lys	Arg	Met	Asn	Ser	Ile	Lys
					565		570
	Arg	Asp	Gln	Tyr	Leu	Met	Trp
55			580			585	
	Lys	Leu	Asn	Glu	Trp	Leu	Gly

148

149

		595				600						605					
		Leu	Val	Glu	Asp	Asp	Glu	Asp	Leu	Pro	His	His	Asp	Glu	Lys	Thr	Trp
		610					615						620				
5		Asn	Val	Gly	Ser	Ser	Asn	Arg	Asn	Lys	Ala	Glu	Asn	Leu	Leu	Arg	Gly
		625					630					635				640	
		Lys	Arg	Asp	Gly	Thr	Phe	Leu	Val	Arg	Glu	Ser	Ser	Lys	Gln	Gly	Cys
						645					650					655	
		Tyr	Ala	Cys	Ser	Val	Val	Val	Asp	Gly	Glu	Val	Lys	His	Cys	Val	Ile
					660				665						670		
10		Asn	Lys	Thr	Ala	Thr	Gly	Tyr	Gly	Phe	Ala	Glu	Pro	Tyr	Asn	Leu	Tyr
					675				680					685			
		Ser	Ser	Leu	Lys	Glu	Leu	Val	Leu	His	Tyr	Gln	His	Thr	Ser	Leu	Val
					690				695					700			
		Gln	His	Asn	Asp	Ser	Leu	Asn	Val	Thr	Leu	Ala	Tyr	Pro	Val	Tyr	Ala
15		705					710					715				720	
		Gln	Gln	Arg	Arg	Gln	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly
						725					730					735	
		Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly
					740				745					750			
20		Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp
					755				760					765			
		Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys
					770				775				780				
		Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val
25		785					790					795				800	
		Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe
						805					810					815	
		Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe
					820				825						830		
30		Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly
					835				840					845			
		Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu
					850				855				860				
		Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His
35		865					870					875				880	
		Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn
						885					890					895	
		Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp
					900				905						910		
40		His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro
					915				920						925		
		Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn
					930				935				940				
		Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly
45		945					950					955				960	
		Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys						
						965					970						

(2) INFORMATION FOR SEQ ID NO:68:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

149

150

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1785

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

10	ATG GGC AAC GCC GCC GCC GCC AAG AAG GGC AGC GAG CAG GAG AGC GTG	48
	Met Gly Asn Ala Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val	
	1 5 10 15	
15	AAA GAG TTC CTA GCC AAA GCC AAG GAA GAT TTC CTG AAA AAA TGG GAA	96
	Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu	
	20 25 30	
20	GAC CCC TCT CAG AAT ACA GCC CAG TTG GAT CAG TTT GAT AGA ATC AAG	144
	Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys	
	35 40 45	
25	ACC CTT GGC ACC GGC TCC TTT GGG CGA GTG ATG CTG GTG AAG CAC AAG	192
	Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys	
	50 55 60	
30	GAG AGT GGG AAC CAC TAC GCC ATG AAG ATC TTA GAC AAG CAG AAG GTG	240
	Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val	
	65 70 75 80	
35	GTG AAG CTA AAG CAG ATC GAG CAC ACT CTG AAT GAG AAG CGC ATC CTG	288
	Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu	
	85 90 95	
40	CAG GCC GTC AAC TTC CCG TTC CTG GTC AAA CTT GAA TTC TCC TTC AAG	336
	Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys	
	100 105 110	
45	GAC AAC TCA AAC CTG TAC ATG GTC ATG GAG TAT GTA GCT GGT GGC GAG	384
	Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Ala Gly Gly Glu	
	115 120 125	
50	ATG TTC TCC CAC CTA CGG CGG ATT GGA AGG TTC AGC GAG CCC CAT GCC	432
	Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala	
	130 135 140	
55	CGT TTC TAC GCG GCG CAG ATC GTC CTG ACC TTT GAG TAT CTG CAC TCC	480
	Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser	
	145 150 155 160	
60	CTG GAC CTC ATC TAC CGG GAC CTG AAG CCC GAG AAT CTT CTC ATC GAC	528
	Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp	
	165 170 175	
65	CAG CAG GGC TAT ATT CAG GTG ACA GAC TTC GGT TTT GCC AAG CGT GTG	576
	Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val	
	180 185 190	

150

151

	AAA GGC CGT ACT TGG ACC TTG TGT GGG ACC CCT GAG TAC TTG GCC CCC	624
	Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro	
	195 200 205	
5	GAG ATT ATC CTG AGC AAA GGC TAC AAC AAG GCT GTG GAC TGG TGG GCT	672
	Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala	
	210 215 220	
10	CTC GGA GTC CTC ATC TAC GAG ATG GCT GCT GGT TAC CCA CCC TTC TTC	720
	Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe	
	225 230 235 240	
15	GCT GAC CAG CCT ATC CAG ATC TAT GAG AAA ATC GTC TCT GGG AAG GTG	768
	Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val	
	245 250 255	
20	CGG TTC CCA TCC CAC TTC AGC TCT GAC TTG AAG GAC CTG CTG CGG AAC	816
	Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn	
	260 265 270	
25	CTT CTG CAA GTG GAT CTA ACC AAG CGC TTT GGA AAC CTC AAG GAC GGG	864
	Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly	
	275 280 285	
30	GTC AAT GAC ATC AAG AAC CAC AAG TGG TTT GCC ACG ACT GAC TGG ATT	912
	Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile	
	290 295 300	
35	GCC ATC TAT CAG AGA AAG GTG GAA GCT CCC TTC ATA CCA AAG TTT AAA	960
	Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys	
	305 310 315 320	
40	GGC CCT GGG GAC ACG AGT AAC TTT GAC GAC TAT GAG GAG GAA GAG ATC	1008
	Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile	
	325 330 335	
45	CGG GTC TCC ATC AAT GAG AAG TGT GGC AAG GAG TTT ACT GAG TTT GGG	1056
	Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly	
	340 345 350	
50	CGC GCC ATG AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT	1104
	Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile	
	355 360 365	
55	CTT GTT GAA TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT AGT	1152
	Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser	
	370 375 380	
60	GGA GAG GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT	1200
	Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe	
	385 390 395 400	
65	ATT TGC ACT ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC ACT	1248
	Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr	
	405 410 415	

151

152

	ACT CTC ACT TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT ATG	1296
	Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met	
	420 425 430	
5	AAA CAG CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG	1344
	Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln	
	435 440 445	
10	GAA AGA ACT ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT	1392
	Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala	
	450 455 460	
15	GAA GTC AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA	1440
	Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys	
	465 470 475 480	
20	GGT ATT GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG GAA	1488
	Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu	
	485 490 495	
25	TAC AAT TAT AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA AAG	1536
	Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys	
	500 505 510	
30	AAT GGC ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT GGA	1584
	Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly	
	515 520 525	
35	AGC GTT CAA TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT	1632
	Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	530 535 540	
40	GGC CCT GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT GCC	1680
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
	545 550 555 560	
45	CTT TCC AAA GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT GAG	1728
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu	
	565 570 575	
50	TTT GTA ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA	1776
	Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
	580 585 590	
55	CCT CAG GAG TAA	1788
	Pro Gln Glu	
	595	

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 595 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

152

153

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

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Met Gly Asn Ala Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val
  1           5           10           15
10  Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu
      20           25           30
    Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys
      35           40           45
15  Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys
      50           55           60
    Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val
      65           70           75           80
    Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu
      85           90           95
20  Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys
      100          105          110
    Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Ala Gly Gly Glu
      115          120          125
25  Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala
      130          135          140
    Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser
      145          150          155          160
    Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp
      165          170          175
30  Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val
      180          185          190
    Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro
      195          200          205
35  Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala
      210          215          220
    Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe
      225          230          235          240
    Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val
      245          250          255
40  Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn
      260          265          270
    Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly
      275          280          285
45  Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile
      290          295          300
    Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys
      305          310          315          320
    Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile
      325          330          335
50  Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly
      340          345          350
    Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
      355          360          365
55  Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
      370          375          380
    Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe

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153

154

385 390 395 400
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 405 410 415
 Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 5 420 425 430
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 435 440 445
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 450 455 460
 10 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 465 470 475 480
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
 485 490 495
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
 15 500 505 510
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
 515 520 525
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 530 535 540
 20 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 545 550 555 560
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
 565 570 575
 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 25 580 585 590
 Pro Gln Glu
 595

(2) INFORMATION FOR SEQ ID NO:70:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2178
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

45

ATG AGC GAC GTG GCT ATT GTG AAG GAG GGT TGG CTG CAC AAA CGA GGG 48
 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
 1 5 10 15

50

GAG TAC ATC AAG ACC TGG CGG CCA CGC TAC TTC CTC CTC AAG AAT GAT 96
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
 20 25 30

55

GGC ACC TTC ATT GGC TAC AAG GAG CGG CCG CAG GAT GTG GAC CAA CGT 144
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
 35 40 45

154

155

	GAG GCT CCC CTC AAC AAC TTC TCT GTG GCG CAG TGC CAG CTG ATG AAG	192
	Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys	
	50 55 60	
5	ACG GAG CGG CCC CGG CCC AAC ACC TTC ATC ATC CGC TGC CTG CAG TGG	240
	Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp	
	65 70 75 80	
10	ACC ACT GTC ATC GAA CGC ACC TTC CAT GTG GAG ACT CCT GAG GAG CGG	288
	Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg	
	85 90 95	
15	GAG GAG TGG ACA ACC GCC ATC CAG ACT GTG GCT GAC GGC CTC AAG AAG	336
	Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys	
	100 105 110	
20	CAG GAG GAG GAG GAG ATG GAC TTC CGG TCG GGC TCA CCC AGT GAC AAC	384
	Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn	
	115 120 125	
25	TCA GGG GCT GAA GAG ATG GAG GTG TCC CTG GCC AAG CCC AAG CAC CGC	432
	Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg	
	130 135 140	
30	GTG ACC ATG AAC GAG TTT GAG TAC CTG AAG CTG CTG GGC AAG GGC ACT	480
	Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr	
	145 150 155 160	
35	TTC GGC AAG GTG ATC CTG GTG AAG GAG AAG GCC ACA GGC CGC TAC TAC	528
	Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr	
	165 170 175	
40	GCC ATG AAG ATC CTC AAG AAG GAA GTC ATC GTG GCC AAG GAC GAG GTG	576
	Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val	
	180 185 190	
45	GCC CAC ACA CTC ACC GAG AAC CGC GTC CTG CAG AAC TCC AGG CAC CCC	624
	Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro	
	195 200 205	
50	TTC CTC ACA GCC CTG AAG TAC TCT TTC CAG ACC CAC GAC CGC CTC TGC	672
	Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys	
	210 215 220	
55	TTT GTC ATG GAG TAC GCC AAC GGG GGC GAG CTG TTC TTC CAC CTG TCC	720
	Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser	
	225 230 235 240	
60	CGG GAA CGT GTG TTC TCC GAG GAC CGG GCC CGC TTC TAT GGC GCT GAG	768
	Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu	
	245 250 255	
65	ATT GTG TCA GCC CTG GAC TAC CTG CAC TCG GAG AAG AAC GTG GTG TAC	816
	Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr	
	260 265 270	

155

156

	CGG GAC CTC AAG CTG GAG AAC CTC ATG CTG GAC AAG GAC GGG CAC ATT	864
	Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile	
	275 280 285	
5	AAG ATC ACA GAC TTC GGG CTG TGC AAG GAG GGG ATC AAG GAC GGT GCC	912
	Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala	
	290 295 300	
10	ACC ATG AAG ACC TTT TGC GGC ACA CCT GAG TAC CTG GCC CCC GAG GTG	960
	Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val	
	305 310 315 320	
15	CTG GAG GAC AAT GAC TAC GGC CGT GCA GTG GAC TGG TGG GGG CTG GGC	1008
	Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly	
	325 330 335	
20	GTG GTC ATG TAC GAG ATG ATG TGC GGT CGC CTG CCC TTC TAC AAC CAG	1056
	Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln	
	340 345 350	
	GAC CAT GAG AAG CTT TTT GAG CTC ATC CTC ATG GAG GAG ATC CGC TTC	1104
	Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe	
	355 360 365	
25	CCG CGC ACG CTT GGT CCC GAG GCC AAG TCC TTG CTT TCA GGG CTG CTC	1152
	Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu	
	370 375 380	
30	AAG AAG GAC CCC AAG CAG AGG CTT GGC GGG GGC TCC GAG GAC GCC AAG	1200
	Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys	
	385 390 395 400	
35	GAG ATC ATG CAG CAT CGC TTC TTT GCC GGT ATC GTG TGG CAG CAC GTG	1248
	Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val	
	405 410 415	
40	TAC GAG AAG AAG CTC AGC CCA CCC TTC AAG CCC CAG GTC ACG TCG GAG	1296
	Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu	
	420 425 430	
	ACT GAC ACC AGG TAT TTT GAT GAG GAG TTC ACG GCC CAG ATG ATC ACC	1344
	Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr	
	435 440 445	
45	ATC ACA CCA CCT GAC CAA GAT GAC AGC ATG GAG TGT GTG GAC AGC GAG	1392
	Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu	
	450 455 460	
50	CGC AGG CCC CAC TTC CCC CAG TTC TCC TAC TCG GCC AGC AGC ACG GCC	1440
	Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala	
	465 470 475 480	
55	TCG GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC	1488
	Ser Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe	
	485 490 495	

156

157

	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	1536
	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	
				500					505					510			
5	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	1584
	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	
			515					520					525				
10	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	1632
	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	
			530					535					540				
15	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	1680
	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	
	545					550					555					560	
20	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	1728
	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	
					565					570					575		
25	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	1776
	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	
				580					585					590			
30	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	1824
	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	
			595					600					605				
35	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	1872
	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	
			610				615					620					
40	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	1920
	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	
	625					630					635					640	
45	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	1968
	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	
					645					650					655		
50	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	2016
	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	
				660					665					670			
55	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	2064
	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	
				675				680					685				
60	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	2112
	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	
				690				695					700				
65	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	2160
	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	
						705		710				715				720	

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ATG GAC GAG CTG TAC AAG TAA
Met Asp Glu Leu Tyr Lys
725

2181

5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 726 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

20 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
1 5 10 15
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
20 25 30
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
25 35 40 45
Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
50 55 60
Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
65 70 75 80
30 Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
85 90 95
Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys
100 105 110
Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
35 115 120 125
Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg
130 135 140
Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
145 150 155 160
40 Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr
165 170 175
Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val
180 185 190
Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro
45 195 200 205
Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys
210 215 220
Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser
225 230 235 240
50 Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu
245 250 255
Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr
260 265 270
Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile
55 275 280 285
Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala

158

159

		290				295				300							
		Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val
		305					310					315				320	
5		Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly
					325						330					335	
		Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln
					340					345					350		
		Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe
					355				360					365			
10		Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu
					370				375					380			
		Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Ser	Glu	Asp	Ala	Lys
							390					395				400	
		Glu	Ile	Met	Gln	His	Arg	Phe	Phe	Ala	Gly	Ile	Val	Trp	Gln	His	Val
15						405					410					415	
		Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu
					420					425					430		
		Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Met	Ile	Thr
					435				440					445			
20		Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Met	Glu	Cys	Val	Asp	Ser	Glu
					450				455				460				
		Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Ser	Thr	Ala
						470						475				480	
		Ser	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe
25						485					490					495	
		Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly
					500					505					510		
		His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly
					515				520					525			
30		Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro
					530				535				540				
		Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser
						550						555				560	
		Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met
35						565					570					575	
		Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly
					580				585					590			
		Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val
					595				600					605			
40		Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile
					610				615					620			
		Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile
						630						635				640	
		Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg
45						645					650					655	
		His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln
					660					665					670		
		Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr
					675				680					685			
50		Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp
					690				695					700			
		His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly
						710						715				720	
55		Met	Asp	Glu	Leu	Tyr	Lys										
						725											

159

160

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2748
 (D) OTHER INFORMATION:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

20	ATG GCT GAC GTT TAC CCG GCC AAC GAC TCC ACG GCG TCT CAG GAC GTG	48
	Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val	
	1 5 10 15	
	GCC AAC CGC TTC GCC CGC AAA GGG GCG CTG AGG CAG AAG AAC GTG CAT	96
	Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His	
	20 25 30	
25	GAG GTG AAA GAC CAC AAA TTC ATC GCC CGC TTC TTC AAG CAA CCC ACC	144
	Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr	
	35 40 45	
30	TTC TGC AGC CAC TGC ACC GAC TTC ATC TGG GGG TTT GGG AAA CAA GGC	192
	Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly	
	50 55 60	
	TTC CAG TGC CAA GTT TGC TGT TTT GTG GTT CAT AAG AGG TGC CAT GAG	240
35	Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu	
	65 70 75 80	
	TTC GTT ACG TTC TCT TGT CCG GGT GCG GAT AAG GGA CCT GAC ACT GAC	288
40	Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp	
	85 90 95	
	GAC CCC AGG AGC AAG CAC AAG TTC AAA ATC CAC ACA TAC GGA AGC CCT	336
	Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro	
	100 105 110	
45	ACC TTC TGT GAT CAC TGT GGG TCC CTG CTC TAT GGA CTT ATC CAC CAA	384
	Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln	
	115 120 125	
50	GGG ATG AAA TGT GAC ACC TGC GAC ATG AAT GTT CAC AAC CAG TGT GTG	432
	Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val	
	130 135 140	
55	ATC AAT GAC CCT AGC CTC TGC GGA ATG GAT CAC ACA GAG AAG AGG GGG	480
	Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly	
	145 150 155 160	

160

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	CGG	ATT	TAT	CTG	AAG	GCT	GAG	GTC	ACT	GAT	GAA	AAG	CTC	CAC	GTC	ACG	528
	Arg	Ile	Tyr	Leu	Lys	Ala	Glu	Val	Thr	Asp	Glu	Lys	Leu	His	Val	Thr	
					165					170					175		
5	GTA	CGA	GAT	GCA	AAA	AAT	CTA	ATC	CCT	ATG	GAT	CCA	AAT	GGG	CTT	TCG	576
	Val	Arg	Asp	Ala	Lys	Asn	Leu	Ile	Pro	Met	Asp	Pro	Asn	Gly	Leu	Ser	
				180					185					190			
10	GAT	CCT	TAT	GTG	AAG	CTG	AAA	CTA	ATC	CCT	GAC	CCC	AAG	AAT	GAG	AGC	624
	Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ile	Pro	Asp	Pro	Lys	Asn	Glu	Ser	
			195					200					205				
15	AAA	CAG	AAA	ACC	AAA	ACC	ATC	CGC	TCC	AAC	CTG	AAT	CCT	CAG	TGG	AAT	672
	Lys	Gln	Lys	Thr	Lys	Thr	Ile	Arg	Ser	Asn	Leu	Asn	Pro	Gln	Trp	Asn	
		210					215					220					
20	GAG	TCC	TTC	ACG	TTC	AAA	TTA	AAA	CCT	TCA	GAC	AAA	GAC	CGG	CGA	CTG	720
	Glu	Ser	Phe	Thr	Phe	Lys	Leu	Lys	Pro	Ser	Asp	Lys	Asp	Arg	Arg	Leu	
	225					230					235					240	
25	TCT	GTA	GAA	ATC	TGG	GAC	TGG	GAT	CGG	ACG	ACT	CGG	AAT	GAC	TTC	ATG	768
	Ser	Val	Glu	Ile	Trp	Asp	Trp	Asp	Arg	Thr	Thr	Arg	Asn	Asp	Phe	Met	
					245				250						255		
30	GGA	TCC	CTT	TCC	TTT	GGT	GTC	TCA	GAG	CTA	ATG	AAG	ATG	CCG	GCC	AGT	816
	Gly	Ser	Leu	Ser	Phe	Gly	Val	Ser	Glu	Leu	Met	Lys	Met	Pro	Ala	Ser	
				260				265						270			
35	CCC	ATT	CCA	GAA	GGA	GAT	GAA	GAA	GGC	AAC	ATG	GAA	CTC	AGG	CAG	AAG	912
	Pro	Ile	Pro	Glu	Gly	Asp	Glu	Glu	Gly	Asn	Met	Glu	Leu	Arg	Gln	Lys	
		290				295						300					
40	TTT	GAG	AAA	GCC	AAG	CTA	GGT	CCT	GTT	GGT	AAC	AAA	GTC	ATC	AGC	CCT	960
	Phe	Glu	Lys	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asn	Lys	Val	Ile	Ser	Pro	
	305					310					315					320	
45	TCA	GAA	GAC	AGA	AAG	CAA	CCA	TCC	AAC	AAC	CTG	GAC	AGA	GTG	AAA	CTC	1008
	Ser	Glu	Asp	Arg	Lys	Gln	Pro	Ser	Asn	Asn	Leu	Asp	Arg	Val	Lys	Leu	
				325					330						335		
50	ACA	GAC	TTC	AAC	TTC	CTC	ATG	GTG	CTG	GGG	AAG	GGG	AGT	TTT	GGG	AAG	1056
	Thr	Asp	Phe	Asn	Phe	Leu	Met	Val	Leu	Gly	Lys	Gly	Ser	Phe	Gly	Lys	
				340					345					350			
55	GTG	ATG	CTT	GCT	GAC	AGG	AAG	GGA	ACG	GAG	GAA	CTG	TAC	GCC	ATC	AAG	1104
	Val	Met	Leu	Ala	Asp	Arg	Lys	Gly	Thr	Glu	Glu	Leu	Tyr	Ala	Ile	Lys	
			355					360					365				
55	ATC	CTG	AAG	AAG	GAC	GTG	GTG	ATC	CAG	GAC	GAC	GAC	GTG	GAG	TGC	ACC	1152
	Ile	Leu	Lys	Lys	Asp	Val	Val	Ile	Gln	Asp	Asp	Asp	Val	Glu	Cys	Thr	
		370						375					380				

161

162

5	ATG GTG GAG AAG CGC GTG CTG GCC CTG CTG GAC AAG CCG CCA TTT CTG	1200
	Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu	
	385 390 395 400	
10	ACA CAG CTG CAC TCC TGC TTC CAG ACA GTG GAC CGG CTG TAC TTC GTC	1248
	Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val	
	405 410 415	
15	ATG GAA TAC GTC AAC GGC GGG GAT CTT ATG TAC CAC ATT CAG CAA GTC	1296
	Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val	
	420 425 430	
20	GGG AAA TTT AAG GAG CCA CAA GCA GTA TTC TAC GCA GCC GAG ATC TCC	1344
	Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser	
	435 440 445	
25	ATC GGA CTG TTC TTC CTT CAT AAA AGA GGG ATC ATT TAC AGG GAT CTG	1392
	Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu	
	450 455 460	
30	AAG CTG AAC AAT GTC ATG CTG AAC TCA GAA GGG CAC ATC AAA ATC GCC	1440
	Lys Leu Asn Asn Val Met Leu Asn Ser Glu Gly His Ile Lys Ile Ala	
	465 470 475 480	
35	GAC TTC GGG ATG TGC AAG GAA CAC ATG ATG GAT GGA GTC ACG ACC AGG	1488
	Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg	
	485 490 495	
40	ACC TTC TGC GGA ACT CCG GAC TAC ATT GCC CCA GAG ATA ATC GCT TAC	1536
	Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr	
	500 505 510	
45	CAG CCG TAC GGG AAG TCT GTA GAT TGG TGG GCG TAC GGT GTG CTG CTG	1584
	Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu	
	515 520 525	
50	TAC GAG ATG CTA GCC GGG CAG CCT CCG TTT GAT GGT GAA GAT GAA GAT	1632
	Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp	
	530 535 540	
55	GAA CTG TTT CAG TCT ATA ATG GAG CAC AAC GTG TCC TAC CCC AAA TCC	1680
	Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser	
	545 550 555 560	
60	TTG TCC AAG GAA GCC GTC TCC ATC TGC AAA GGA CTT ATG ACC AAA CAG	1728
	Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys Gln	
	565 570 575	
65	CCT GCC AAG CGA CTG GGC TGC GGG CCC GAG GGA GAG AGG GAT GTC AGA	1776
	Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg	
	580 585 590	
70	GAG CAT GCC TTC TTC AGG AGG ATC GAC TGG GAG AAA CTG GAG AAC AGG	1824
	Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg	
	595 600 605	

162

	GAG ATC CAA CCA CCA TTC AAG CCC AAA GTG TGT GGC AAA GGA GCA GAA	1872
	Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu	
	610 615 620	
5	AAC TTT GAC AAG TTC TTC ACG CGA GGA CAG CCT GTC TTA ACA CCA CCA	1920
	Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro	
	625 630 635 640	
10	GAT CAG CTG GTC ATT GCT AAC ATA GAC CAA TCT GAT TTT GAA GGG TTC	1968
	Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe	
	645 650 655	
15	TCG TAT GTC AAC CCC CAG TTT GTG CAC CCA ATC TTG CAA AGT GCA GTA	2016
	Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val	
	660 665 670	
20	GGG CGC GCC ATG AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA	2064
	Gly Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro	
	675 680 685	
25	ATT CTT GTT GAA TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT	2112
	Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val	
	690 695 700	
30	AGT GGA GAG GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA	2160
	Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	
	705 710 715 720	
35	TTT ATT TGC ACT ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC	2208
	Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val	
	725 730 735	
40	ACT ACT CTC ACT TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT	2256
	Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His	
	740 745 750	
45	ATG AAA CAG CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA	2304
	Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val	
	755 760 765	
50	CAG GAA AGA ACT ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT	2352
	Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg	
	770 775 780	
55	GCT GAA GTC AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA	2400
	Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu	
	785 790 795 800	
60	AAA GGT ATT GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG	2448
	Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met	
	805 810 815	
65	GAA TAC AAT TAT AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA	2496
	Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro	
	820 825 830	

164

5 AAG AAT GGC ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT 2544
 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp
 835 840 845
 GGA AGC GTT CAA TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC 2592
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 850 855 860
 10 GAT GGC CCT GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT 2640
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 865 870 875 880
 15 GCC CTT TCC AAA GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT 2688
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu
 885 890 895
 20 GAG TTT GTA ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC 2736
 Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr
 900 905 910
 AAA CCT CAG GAG TAA 2751
 Lys Pro Gln Glu
 915

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 916 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

40 Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val
 1 5 10 15
 Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His
 20 25 30
 45 Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr
 35 40 45
 Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly
 50 55 60
 Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu
 65 70 75 80
 50 Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp
 85 90 95
 Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro
 100 105 110
 55 Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln
 115 120 125
 Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val

164

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	130		135		140														
	Ile	Asn	Asp	Pro	Ser	Leu	Cys	Gly	Met	Asp	His	Thr	Glu	Lys	Arg	Gly			
	145					150					155					160			
	Arg	Ile	Tyr	Leu	Lys	Ala	Glu	Val	Thr	Asp	Glu	Lys	Leu	His	Val	Thr			
5					165					170					175				
	Val	Arg	Asp	Ala	Lys	Asn	Leu	Ile	Pro	Met	Asp	Pro	Asn	Gly	Leu	Ser			
				180					185					190					
	Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ile	Pro	Asp	Pro	Lys	Asn	Glu	Ser			
		195						200					205						
10	Lys	Gln	Lys	Thr	Lys	Thr	Ile	Arg	Ser	Asn	Leu	Asn	Pro	Gln	Trp	Asn			
	210						215						220						
	Glu	Ser	Phe	Thr	Phe	Lys	Leu	Lys	Pro	Ser	Asp	Lys	Asp	Arg	Arg	Leu			
	225					230					235					240			
	Ser	Val	Glu	Ile	Trp	Asp	Trp	Asp	Arg	Thr	Thr	Arg	Asn	Asp	Phe	Met			
15					245					250					255				
	Gly	Ser	Leu	Ser	Phe	Gly	Val	Ser	Glu	Leu	Met	Lys	Met	Pro	Ala	Ser			
				260					265					270					
	Gly	Trp	Tyr	Lys	Ala	His	Asn	Gln	Glu	Glu	Gly	Glu	Tyr	Tyr	Asn	Val			
		275						280					285						
20	Pro	Ile	Pro	Glu	Gly	Asp	Glu	Glu	Gly	Asn	Met	Glu	Leu	Arg	Gln	Lys			
	290						295					300							
	Phe	Glu	Lys	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asn	Lys	Val	Ile	Ser	Pro			
	305					310					315					320			
	Ser	Glu	Asp	Arg	Lys	Gln	Pro	Ser	Asn	Asn	Leu	Asp	Arg	Val	Lys	Leu			
25					325					330					335				
	Thr	Asp	Phe	Asn	Phe	Leu	Met	Val	Leu	Gly	Lys	Gly	Ser	Phe	Gly	Lys			
				340					345					350					
	Val	Met	Leu	Ala	Asp	Arg	Lys	Gly	Thr	Glu	Glu	Leu	Tyr	Ala	Ile	Lys			
		355						360					365						
30	Ile	Leu	Lys	Lys	Asp	Val	Val	Ile	Gln	Asp	Asp	Asp	Val	Glu	Cys	Thr			
	370						375					380							
	Met	Val	Glu	Lys	Arg	Val	Leu	Ala	Leu	Leu	Asp	Lys	Pro	Pro	Phe	Leu			
	385					390					395					400			
	Thr	Gln	Leu	His	Ser	Cys	Phe	Gln	Thr	Val	Asp	Arg	Leu	Tyr	Phe	Val			
35					405					410					415				
	Met	Glu	Tyr	Val	Asn	Gly	Gly	Asp	Leu	Met	Tyr	His	Ile	Gln	Gln	Val			
				420					425				430						
	Gly	Lys	Phe	Lys	Glu	Pro	Gln	Ala	Val	Phe	Tyr	Ala	Ala	Glu	Ile	Ser			
		435					440					445							
40	Ile	Gly	Leu	Phe	Phe	Leu	His	Lys	Arg	Gly	Ile	Ile	Tyr	Arg	Asp	Leu			
	450					455					460								
	Lys	Leu	Asn	Asn	Val	Met	Leu	Asn	Ser	Glu	Gly	His	Ile	Lys	Ile	Ala			
	465					470					475					480			
	Asp	Phe	Gly	Met	Cys	Lys	Glu	His	Met	Met	Asp	Gly	Val	Thr	Thr	Arg			
45					485					490					495				
	Thr	Phe	Cys	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Ile	Ile	Ala	Tyr			
				500					505				510						
	Gln	Pro	Tyr	Gly	Lys	Ser	Val	Asp	Trp	Trp	Ala	Tyr	Gly	Val	Leu	Leu			
		515						520					525						
50	Tyr	Glu	Met	Leu	Ala	Gly	Gln	Pro	Pro	Phe	Asp	Gly	Glu	Asp	Glu	Asp			
	530						535					540							
	Glu	Leu	Phe	Gln	Ser	Ile	Met	Glu	His	Asn	Val	Ser	Tyr	Pro	Lys	Ser			
	545					550					555					560			
	Leu	Ser	Lys	Glu	Ala	Val	Ser	Ile	Cys	Lys	Gly	Leu	Met	Thr	Lys	Gln			
55					565					570					575				
	Pro	Ala	Lys	Arg	Leu	Gly	Cys	Gly	Pro	Glu	Gly	Glu	Arg	Asp	Val	Arg			

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				580				585					590			
	Glu	His	Ala	Phe	Phe	Arg	Arg	Ile	Asp	Trp	Glu	Lys	Leu	Glu	Asn	Arg
			595					600					605			
	Glu	Ile	Gln	Pro	Pro	Phe	Lys	Pro	Lys	Val	Cys	Gly	Lys	Gly	Ala	Glu
5		610					615					620				
	Asn	Phe	Asp	Lys	Phe	Phe	Thr	Arg	Gly	Gln	Pro	Val	Leu	Thr	Pro	Pro
	625					630					635				640	
	Asp	Gln	Leu	Val	Ile	Ala	Asn	Ile	Asp	Gln	Ser	Asp	Phe	Glu	Gly	Phe
				645					650					655		
10	Ser	Tyr	Val	Asn	Pro	Gln	Phe	Val	His	Pro	Ile	Leu	Gln	Ser	Ala	Val
				660					665					670		
	Gly	Arg	Ala	Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro
			675					680					685			
	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val
15		690					695					700				
	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys
	705					710					715				720	
	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val
				725					730					735		
20	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His
				740					745					750		
	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val
			755					760					765			
	Gln	Glu	Arg	Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg
25		770					775					780				
	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu
	785					790					795				800	
	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met
				805					810					815		
30	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro
			820						825					830		
	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp
			835					840					845			
	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly
35		850					855					860				
	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser
	865					870					875				880	
	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu
				885					890					895		
40	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr
				900					905					910		
	Lys	Pro	Gln	Glu												
				915												

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(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2157 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

55

(A) NAME/KEY: Coding Sequence

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(B) LOCATION: 1...2154

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

5	ATG TCG TCC ATC TTG CCA TTC ACG CCG CCA GTT GTG AAG AGA CTG CTG	48
	Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu	
	1 5 10 15	
10	GGA TGG AAG AAG TCA GCT GGT GGG TCT GGA GGA GCA GGC GGA GGA GAG	96
	Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu	
	20 25 30	
15	CAG AAT GGG CAG GAA GAA AAG TGG TGT GAG AAA GCA GTG AAA AGT CTG	144
	Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu	
	35 40 45	
20	GTG AAG AAG CTA AAG AAA ACA GGA CGA TTA GAT GAG CTT GAG AAA GCC	192
	Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala	
	50 55 60	
25	ATC ACC ACT CAA AAC TGT AAT ACT AAA TGT GTT ACC ATA CCA AGC ACT	240
	Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr	
	65 70 75 80	
30	TGC TCT GAA ATT TGG GGA CTG AGT ACA CCA AAT ACG ATA GAT CAG TGG	288
	Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp	
	85 90 95	
35	GAT ACA ACA GGC CTT TAC AGC TTC TCT GAA CAA ACC AGG TCT CTT GAT	336
	Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp	
	100 105 110	
40	GGT CGT CTC CAG GTA TCC CAT CGA AAA GGA TTG CCA CAT GTT ATA TAT	384
	Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr	
	115 120 125	
45	TGC CGA TTA TGG CGC TGG CCT GAT CTT CAC AGT CAT CAT GAA CTC AAG	432
	Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys	
	130 135 140	
50	GCA ATT GAA AAC TGC GAA TAT GCT TTT AAT CTT AAA AAG GAT GAA GTA	480
	Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val	
	145 150 155 160	
55	TGT GTA AAC CCT TAC CAC TAT CAG AGA GTT GAG ACA CCA GTT TTG CCT	528
	Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro	
	165 170 175	
60	CCA GTA TTA GTG CCC CGA CAC ACC GAG ATC CTA ACA GAA CTT CCG CCT	576
	Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro	
	180 185 190	
65	CTG GAT GAC TAT ACT CAC TCC ATT CCA GAA AAC ACT AAC TTC CCA GCA	624
	Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala	
	195 200 205	

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	GGA ATT GAG CCA CAG AGT AAT TAT ATT CCA GAA ACG CCA CCT CCT GGA	672
	Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly	
	210 215 220	
5	TAT ATC AGT GAA GAT GGA GAA ACA AGT GAC CAA CAG TTG AAT CAA AGT	720
	Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser	
	225 230 235 240	
10	ATG GAC ACA GGC TCT CCA GCA GAA CTA TCT CCT ACT ACT CTT TCC CCT	768
	Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro	
	245 250 255	
15	GTT AAT CAT AGC TTG GAT TTA CAG CCA GTT ACT TAC TCA GAA CCT GCA	816
	Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala	
	260 265 270	
20	TTT TGG TGT TCA ATA GCA TAT TAT GAA TTA AAT CAG AGG GTT GGA GAA	864
	Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu	
	275 280 285	
25	ACC TTC CAT GCA TCA CAG CCC TCA CTC ACT GTA GAT GGC TTT ACA GAC	912
	Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp	
	290 295 300	
30	CCA TCA AAT TCA GAG AGG TTC TGC TTA GGT TTA CTC TCC AAT GTT AAC	960
	Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn	
	305 310 315 320	
35	CGA AAT GCC ACG GTA GAA ATG ACA AGA AGG CAT ATA GGA AGA GGA GTG	1008
	Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val	
	325 330 335	
40	CGC TTA TAC TAC ATA GGT GGG GAA GTT TTT GCT GAG TGC CTA AGT GAT	1056
	Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp	
	340 345 350	
45	AGT GCA ATC TTT GTG CAG AGC CCC AAT TGT AAT CAG AGA TAT GGC TGG	1104
	Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp	
	355 360 365	
50	CAC CCT GCA ACA GTG TGT AAA ATT CCA CCA GGC TGT AAT CTG AAG ATC	1152
	His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile	
	370 375 380	
55	TTC AAC AAC CAG GAA TTT GCT GCT CTT CTG GCT CAG TCT GTT AAT CAG	1200
	Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln	
	385 390 395 400	
55	GGT TTT GAA GCC GTC TAT CAG CTA ACT AGA ATG TGC ACC ATA AGA ATG	1248
	Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met	
	405 410 415	
55	AGT TTT GTG AAA GGG TGG GGA GCA GAA TAC CGA AGG CAG ACG GTA ACA	1296
	Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr	
	420 425 430	

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	AGT	ACT	CCT	TGC	TGG	ATT	GAA	CTT	CAT	CTG	AAT	GGA	CCT	CTA	CAG	TGG	1344
	Ser	Thr	Pro	Cys	Trp	Ile	Glu	Leu	His	Leu	Asn	Gly	Pro	Leu	Gln	Trp	
			435					440					445				
5	TTG	GAC	AAA	GTA	TTA	ACT	CAG	ATG	GGA	TCC	CCT	TCA	GTG	CGT	TGC	TCA	1392
	Leu	Asp	Lys	Val	Leu	Thr	Gln	Met	Gly	Ser	Pro	Ser	Val	Arg	Cys	Ser	
		450					455					460					
10	AGC	ATG	TCA	TGG	GTA	CCG	CGG	GCC	CGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	1440
	Ser	Met	Ser	Trp	Val	Pro	Arg	Ala	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	
	465					470					475					480	
15	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	1488
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
				485						490					495		
20	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	1536
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				500					505					510			
25	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	1584
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			515					520					525				
30	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	1632
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
			530				535					540					
35	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	1680
	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
	545					550					555					560	
40	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	1728
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					565					570					575		
45	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	1776
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			580					585					590				
50	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	1824
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			595				600					605					
55	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	1872
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		610					615					620					
60	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	1920
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
	625					630					635					640	
65	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	1968
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
				645						650					655		

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5 CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC 2016
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 660 665 670
 GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC 2064
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 675 680 685
 10 AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG 2112
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 690 695 700
 15 ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 2157
 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
 1 5 10 15
 Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu
 20 25 30
 Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
 35 40 45
 Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala
 50 55 60
 Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
 65 70 75 80
 Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp
 85 90 95
 Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
 100 105 110
 Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
 115 120 125
 Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
 130 135 140
 50 Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
 145 150 155 160
 Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
 165 170 175
 Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro
 180 185 190
 55 Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala

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		195				200				205							
	Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly	
		210					215					220					
5	Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser	
	225					230					235					240	
	Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro	
					245					250					255		
	Val	Asn	His	Ser	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala	
				260					265					270			
10	Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu	
			275					280					285				
	Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp	
		290					295					300					
15	Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn	
	305					310					315					320	
	Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val	
					325				330						335		
	Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp	
				340					345					350			
20	Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp	
			355					360					365				
	His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile	
		370					375					380					
25	Phe	Asn	Asn	Gln	Glu	Phe	Ala	Ala	Leu	Leu	Ala	Gln	Ser	Val	Asn	Gln	
	385					390					395					400	
	Gly	Phe	Glu	Ala	Val	Tyr	Gln	Leu	Thr	Arg	Met	Cys	Thr	Ile	Arg	Met	
					405					410					415		
	Ser	Phe	Val	Lys	Gly	Trp	Gly	Ala	Glu	Tyr	Arg	Arg	Gln	Thr	Val	Thr	
				420					425					430			
30	Ser	Thr	Pro	Cys	Trp	Ile	Glu	Leu	His	Leu	Asn	Gly	Pro	Leu	Gln	Trp	
			435					440					445				
	Leu	Asp	Lys	Val	Leu	Thr	Gln	Met	Gly	Ser	Pro	Ser	Val	Arg	Cys	Ser	
		450					455					460					
35	Ser	Met	Ser	Trp	Val	Pro	Arg	Ala	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	
	465					470					475					480	
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
					485					490					495		
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				500					505					510			
40	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			515					520					525				
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
		530					535					540					
	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
45	545					550					555					560	
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					565					570					575		
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				580					585					590			
50	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			595					600					605				
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		610					615					620					
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
55	625					630					635					640	
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	

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645 650 655
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 660 665 670
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 675 680 685
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 690 695 700
 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2394
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GAC AAT ATG TCT ATT ACG AAT ACA CCA ACA AGT AAT GAT GCC TGT 48
 Met Asp Asn Met Ser Ile Thr Asn Thr Pro Thr Ser Asn Asp Ala Cys
 1 5 10 15
 CTG AGC ATT GTG CAT AGT TTG ATG TGC CAT AGA CAA GGT GGA GAG AGT 96
 Leu Ser Ile Val His Ser Leu Met Cys His Arg Gln Gly Gly Glu Ser
 20 25 30
 GAA ACA TTT GCA AAA AGA GCA ATT GAA AGT TTG GTA AAG AAG CTG AAG 144
 Glu Thr Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys
 35 40 45
 GAG AAA AAA GAT GAA TTG GAT TCT TTA ATA ACA GCT ATA ACT ACA AAT 192
 Glu Lys Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn
 50 55 60
 GGA GCT CAT CCT AGT AAA TGT GTT ACC ATA CAG AGA ACA TTG GAT GGG 240
 Gly Ala His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly
 65 70 75 80
 AGG CTT CAG GTG GCT GGT CGG AAA GGA TTT CCT CAT GTG ATC TAT GCC 288
 Arg Leu Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala
 85 90 95
 CGT CTC TGG AGG TGG CCT GAT CTT CAC AAA AAT GAA CTA AAA CAT GTT 336
 Arg Leu Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val
 100 105 110
 AAA TAT TGT CAG TAT GCG TTT GAC TTA AAA TGT GAT AGT GTC TGT GTG 384

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	Lys	Tyr	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val	
			115					120					125				
5	AAT	CCA	TAT	CAC	TAC	GAA	CGA	GTT	GTA	TCA	CCT	GGA	ATT	GAT	CTC	TCA	432
	Asn	Pro	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser	
		130					135					140					
10	GGA	TTA	ACA	CTG	CAG	AGT	AAT	GCT	CCA	TCA	AGT	ATG	ATG	GTG	AAG	GAT	480
	Gly	Leu	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp	
	145					150					155					160	
15	GAA	TAT	GTG	CAT	GAC	TTT	GAG	GGA	CAG	CCA	TCG	TTG	TCC	ACT	GAA	GGA	528
	Glu	Tyr	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly	
					165					170					175		
	CAT	TCA	ATT	CAA	ACC	ATC	CAG	CAT	CCA	CCA	AGT	AAT	CGT	GCA	TCG	ACA	576
	His	Ser	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr	
				180					185					190			
20	GAG	ACA	TAC	AGC	ACC	CCA	GCT	CTG	TTA	GCC	CCA	TCT	GAG	TCT	AAT	GCT	624
	Glu	Thr	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala	
		195					200						205				
25	ACC	AGC	ACT	GCC	AAC	TTT	CCC	AAC	ATT	CCT	GTG	GCT	TCC	ACA	AGT	CAG	672
	Thr	Ser	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln	
		210					215					220					
30	CCT	GCC	AGT	ATA	CTG	GGG	GGC	AGC	CAT	AGT	GAA	GGA	CTG	TTG	CAG	ATA	720
	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile	
	225					230					235				240		
35	GCA	TCA	GGG	CCT	CAG	CCA	GGA	CAG	CAG	CAG	AAT	GGA	TTT	ACT	GGT	CAG	768
	Ala	Ser	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln	
					245					250					255		
	CCA	GCT	ACT	TAC	CAT	CAT	AAC	AGC	ACT	ACC	ACC	TGG	ACT	GGA	AGT	AGG	816
	Pro	Ala	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg	
				260					265					270			
40	ACT	GCA	CCA	TAC	ACA	CCT	AAT	TTG	CCT	CAC	CAC	CAA	AAC	GGC	CAT	CTT	864
	Thr	Ala	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu	
		275					280						285				
45	CAG	CAC	CAC	CCG	CCT	ATG	CCG	CCC	CAT	CCC	GGA	CAT	TAC	TGG	CCT	GTT	912
	Gln	His	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val	
		290					295				300						
50	CAC	AAT	GAG	CTT	GCA	TTC	CAG	CCT	CCC	ATT	TCC	AAT	CAT	CCT	GCT	CCT	960
	His	Asn	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro	
	305					310				315					320		
55	GAG	TAT	TGG	TGT	TCC	ATT	GCT	TAC	TTT	GAA	ATG	GAT	GTT	CAG	GTA	GGA	1008
	Glu	Tyr	Trp	Cys	Ser	Ile	Ala	Tyr	Phe	Glu	Met	Asp	Val	Gln	Val	Gly	
					325					330					335		
	GAG	ACA	TTT	AAG	GTT	CCT	TCA	AGC	TGC	CCT	ATT	GTT	ACT	GTT	GAT	GGA	1056

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	Glu	Thr	Phe	Lys	Val	Pro	Ser	Ser	Cys	Pro	Ile	Val	Thr	Val	Asp	Gly	
				340					345						350		
5	TAC	GTG	GAC	CCT	TCT	GGA	GGA	GAT	CGC	TTT	TGT	TTG	GGT	CAA	CTC	TCC	1104
	Tyr	Val	Asp	Pro	Ser	Gly	Gly	Asp	Arg	Phe	Cys	Leu	Gly	Gln	Leu	Ser	
			355					360					365				
10	AAT	GTC	CAC	AGG	ACA	GAA	GCC	ATT	GAG	AGA	GCA	AGG	TTG	CAC	ATA	GGC	1152
	Asn	Val	His	Arg	Thr	Glu	Ala	Ile	Glu	Arg	Ala	Arg	Leu	His	Ile	Gly	
		370					375					380					
15	AAA	GGT	GTG	CAG	TTG	GAA	TGT	AAA	GGT	GAA	GGT	GAT	GTT	TGG	GTC	AGG	1200
	Lys	Gly	Val	Gln	Leu	Glu	Cys	Lys	Gly	Glu	Gly	Asp	Val	Trp	Val	Arg	
	385					390				395					400		
	TGC	CTT	AGT	GAC	CAC	GCG	GTC	TTT	GTA	CAG	AGT	TAC	TAC	TTA	GAC	AGA	1248
	Cys	Leu	Ser	Asp	His	Ala	Val	Phe	Val	Gln	Ser	Tyr	Tyr	Leu	Asp	Arg	
					405					410					415		
20	GAA	GCT	GGG	CGT	GCA	CCT	GGA	GAT	GCT	GTT	CAT	AAG	ATC	TAC	CCA	AGT	1296
	Glu	Ala	Gly	Arg	Ala	Pro	Gly	Asp	Ala	Val	His	Lys	Ile	Tyr	Pro	Ser	
				420					425					430			
25	GCA	TAT	ATA	AAG	GTC	TTT	GAT	TTG	CGT	CAG	TGT	CAT	CGA	CAG	ATG	CAG	1344
	Ala	Tyr	Ile	Lys	Val	Phe	Asp	Leu	Arg	Gln	Cys	His	Arg	Gln	Met	Gln	
		435						440					445				
30	CAG	CAG	GCG	GCT	ACT	GCA	CAA	GCT	GCA	GCA	GCT	GCC	CAG	GCA	GCA	GCC	1392
	Gln	Gln	Ala	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Ala	Ala	Gln	Ala	Ala	Ala	
		450					455					460					
35	GTG	GCA	GGA	AAC	ATC	CCT	GGC	CCA	GGA	TCA	GTA	GGT	GGA	ATA	GCT	CCA	1440
	Val	Ala	Gly	Asn	Ile	Pro	Gly	Pro	Gly	Ser	Val	Gly	Gly	Ile	Ala	Pro	
	465					470					475				480		
	GCT	ATC	AGT	CTG	TCA	GCT	GCT	GCT	GGA	ATT	GGT	GTT	GAT	GAC	CTT	CGT	1488
	Ala	Ile	Ser	Leu	Ser	Ala	Ala	Ala	Gly	Ile	Gly	Val	Asp	Asp	Leu	Arg	
					485					490					495		
40	CGC	TTA	TGC	ATA	CTC	AGG	ATG	AGT	TTT	GTG	AAA	GGC	TGG	GGA	CCG	GAT	1536
	Arg	Leu	Cys	Ile	Leu	Arg	Met	Ser	Phe	Val	Lys	Gly	Trp	Gly	Pro	Asp	
				500					505					510			
45	TAC	CCA	AGA	CAG	AGC	ATC	AAA	GAA	ACA	CCT	TGC	TGG	ATT	GAA	ATT	CAC	1584
	Tyr	Pro	Arg	Gln	Ser	Ile	Lys	Glu	Thr	Pro	Cys	Trp	Ile	Glu	Ile	His	
			515					520					525				
50	TTA	CAC	CGG	GCC	CTC	CAG	CTC	CTA	GAC	GAA	GTA	CTT	CAT	ACC	ATG	CCG	1632
	Leu	His	Arg	Ala	Leu	Gln	Leu	Leu	Asp	Glu	Val	Leu	His	Thr	Met	Pro	
		530					535					540					
55	ATT	GCA	GAC	CCA	CAA	CCT	TTA	GAC	TGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	1680
	Ile	Ala	Asp	Pro	Gln	Pro	Leu	Asp	Trp	Asp	Pro	Pro	Val	Ala	Thr	Met	
	545					550					555				560		
	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	1728

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	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
					565					570					575		
5	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	1776
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
				580				585					590				
10	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	1824
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			595					600					605				
15	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	1872
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
			610				615					620					
20	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	1920
	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
	625					630					635				640		
25	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	1968
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
					645					650					655		
30	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	2016
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				660				665						670			
35	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	2064
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
			675				680						685				
40	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	2112
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
			690				695					700					
45	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	2160
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
	705					710					715				720		
50	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	2208
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
					725					730				735			
55	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	2256
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
				740					745				750				
60	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	2304
	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
			755					760					765				
65	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG	2352
	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	
		770					775					780					
70	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TAA		2397

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Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 785 790 795

5 (2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

	Met	Asp	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys
	1			5						10					15	
20	Leu	Ser	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser
			20						25					30		
	Glu	Thr	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys
			35					40					45			
25	Glu	Lys	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn
		50					55					60				
	Gly	Ala	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly
	65					70					75				80	
	Arg	Leu	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala
				85					90						95	
30	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val
			100						105					110		
	Lys	Tyr	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val
			115					120					125			
35	Asn	Pro	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser
		130					135					140				
	Gly	Leu	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp
	145					150					155				160	
	Glu	Tyr	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly
				165					170					175		
40	His	Ser	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr
			180						185					190		
	Glu	Thr	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala
		195						200					205			
45	Thr	Ser	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln
		210						215					220			
	Pro	Ala	Ser	Ile	Leu	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile	
	225				230					235				240		
	Ala	Ser	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln
				245					250					255		
50	Pro	Ala	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg
			260						265					270		
	Thr	Ala	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu
		275						280					285			
	Gln	His	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val
55		290					295					300				
	His	Asn	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro

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	305		310		315		320
	Glu Tyr Trp Cys Ser	Ile Ala Tyr Phe	Glu Met Asp Val	Gln Val Gly			
		325	330		335		
5	Glu Thr Phe Lys Val	Pro Ser Ser Cys	Pro Ile Val Thr	Val Asp Gly			
		340	345		350		
	Tyr Val Asp Pro Ser	Gly Gly Asp Arg	Phe Cys Leu Gly	Gln Leu Ser			
		355	360		365		
	Asn Val His Arg Thr	Glu Ala Ile Glu	Arg Ala Arg Leu	His Ile Gly			
		370	375		380		
10	Lys Gly Val Gln Leu	Glu Cys Lys Gly	Glu Gly Asp Val	Trp Val Arg			
		385	390		395		400
	Cys Leu Ser Asp His	Ala Val Phe Val	Gln Ser Tyr Tyr	Leu Asp Arg			
		405	410		415		
	Glu Ala Gly Arg Ala	Pro Gly Asp Ala	Val His Lys Ile	Tyr Pro Ser			
15		420	425		430		
	Ala Tyr Ile Lys Val	Phe Asp Leu Arg	Gln Cys His Arg	Gln Met Gln			
		435	440		445		
	Gln Gln Ala Ala Thr	Ala Gln Ala Ala	Ala Ala Ala Gln	Ala Ala Ala			
		450	455		460		
20	Val Ala Gly Asn Ile	Pro Gly Pro Gly	Ser Val Gly Gly	Ile Ala Pro			
		465	470		475		480
	Ala Ile Ser Leu Ser	Ala Ala Ala Gly	Ile Gly Val Asp	Asp Leu Arg			
		485	490		495		
	Arg Leu Cys Ile Leu	Arg Met Ser Phe	Val Lys Gly Trp	Gly Pro Asp			
25		500	505		510		
	Tyr Pro Arg Gln Ser	Ile Lys Glu Thr	Pro Cys Trp Ile	Glu Ile His			
		515	520		525		
	Leu His Arg Ala Leu	Gln Leu Leu Asp	Glu Val Leu His	Thr Met Pro			
		530	535		540		
30	Ile Ala Asp Pro Gln	Pro Leu Asp Trp	Asp Pro Pro Val	Ala Thr Met			
		545	550		555		560
	Val Ser Lys Gly Glu	Glu Leu Phe Thr	Gly Val Val Pro	Ile Leu Val			
		565	570		575		
	Glu Leu Asp Gly Asp	Val Asn Gly His	Lys Phe Ser Val	Ser Gly Glu			
35		580	585		590		
	Gly Glu Gly Asp Ala	Thr Tyr Gly Lys	Leu Thr Leu Lys	Phe Ile Cys			
		595	600		605		
	Thr Thr Gly Lys Leu	Pro Val Pro Trp	Pro Thr Leu Val	Thr Thr Leu			
		610	615		620		
40	Thr Tyr Gly Val Gln	Cys Phe Ser Arg	Tyr Pro Asp His	Met Lys Gln			
		625	630		635		640
	His Asp Phe Phe Lys	Ser Ala Met Pro	Glu Gly Tyr Val	Gln Glu Arg			
		645	650		655		
	Thr Ile Phe Phe Lys	Asp Asp Gly Asn	Tyr Lys Thr Arg	Ala Glu Val			
45		660	665		670		
	Lys Phe Glu Gly Asp	Thr Leu Val Asn	Arg Ile Glu Leu	Lys Gly Ile			
		675	680		685		
	Asp Phe Lys Glu Asp	Gly Asn Ile Leu	Gly His Lys Leu	Glu Tyr Asn			
		690	695		700		
50	Tyr Asn Ser His Asn	Val Tyr Ile Met	Ala Asp Lys Gln	Lys Asn Gly			
		705	710		715		720
	Ile Lys Val Asn Phe	Lys Ile Arg His	Asn Ile Glu Asp	Gly Ser Val			
		725	730		735		
	Gln Leu Ala Asp His	Tyr Gln Gln Asn	Thr Pro Ile Gly	Asp Gly Pro			
55		740	745		750		
	Val Leu Leu Pro Asp	Asn His Tyr Leu	Ser Thr Gln Ser	Ala Leu Ser			

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	755		760		765
	Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val				
	770		775		780
	Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys				
5	785		790		795

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 3138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...3135
 20 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

25	ATG GCG GGC TGG ATC CAG GCC CAG CAG CTG CAG GGA GAC GCG CTG CGC	48
	Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln Gly Asp Ala Leu Arg	
	1 5 10 15	
30	CAG ATG CAG GTG CTG TAC GGC CAG CAC TTC CCC ATC GAG GTC CGG CAC	96
	Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His	
	20 25 30	
35	TAC TTG GCC CAG TGG ATT GAG AGC CAG CCA TGG GAT GCC ATT GAC TTG	144
	Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu	
	35 40 45	
40	GAC AAT CCC CAG GAC AGA GCC CAA GCC ACC CAG CTC CTG GAG GGC CTG	192
	Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu	
	50 55 60	
45	GTG CAG GAG CTG CAG AAG AAG GCG GAG CAC CAG GTG GGG GAA GAT GGG	240
	Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly	
	65 70 75 80	
50	TTT TTA CTG AAG ATC AAG CTG GGG CAC TAC GCC ACG CAG CTC CAG AAA	288
	Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys	
	85 90 95	
55	ACA TAT GAC CGC TGC CCC CTG GAG CTG GTC CGC TGC ATC CGG CAC ATT	336
	Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile	
	100 105 110	
55	CTG TAC AAT GAA CAG AGG CTG GTC CGA GAA GCC AAC AAT TGC AGC TCT	384
	Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser	
	115 120 125	
55	CCG GCT GGG ATC CTG GTT GAC GCC ATG TCC CAG AAG CAC CTT CAG ATC	432

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	Pro	Ala	Gly	Ile	Leu	Val	Asp	Ala	Met	Ser	Gln	Lys	His	Leu	Gln	Ile	
	130						135					140					
5	AAC	CAG	ACA	TTT	GAG	GAG	CTG	CGA	CTG	GTC	ACG	CAG	GAC	ACA	GAG	AAT	480
	Asn	Gln	Thr	Phe	Glu	Glu	Leu	Arg	Leu	Val	Thr	Gln	Asp	Thr	Glu	Asn	
	145				150					155					160		
10	GAG	CTG	AAG	AAA	CTG	CAG	CAG	ACT	CAG	GAG	TAC	TTC	ATC	ATC	CAG	TAC	528
	Glu	Leu	Lys	Lys	Leu	Gln	Gln	Thr	Gln	Glu	Tyr	Phe	Ile	Ile	Gln	Tyr	
					165					170					175		
15	CAG	GAG	AGC	CTG	AGG	ATC	CAA	GCT	CAG	TTT	GCC	CAG	CTG	GCC	CAG	CTG	576
	Gln	Glu	Ser	Leu	Arg	Ile	Gln	Ala	Gln	Phe	Ala	Gln	Leu	Ala	Gln	Leu	
					180				185					190			
20	AGC	CCC	CAG	GAG	CGT	CTG	AGC	CGG	GAG	ACG	GCC	CTC	CAG	CAG	AAG	CAG	624
	Ser	Pro	Gln	Glu	Arg	Leu	Ser	Arg	Glu	Thr	Ala	Leu	Gln	Gln	Lys	Gln	
			195					200					205				
25	GTG	TCT	CTG	GAG	GCC	TGG	TTG	CAG	CGT	GAG	GCA	CAG	ACA	CTG	CAG	CAG	672
	Val	Ser	Leu	Glu	Ala	Trp	Leu	Gln	Arg	Glu	Ala	Gln	Thr	Leu	Gln	Gln	
	210						215					220					
30	TAC	CGC	GTG	GAG	CTG	GCC	GAG	AAG	CAC	CAG	AAG	ACC	CTG	CAG	CTG	CTG	720
	Tyr	Arg	Val	Glu	Leu	Ala	Glu	Lys	His	Gln	Lys	Thr	Leu	Gln	Leu	Leu	
	225					230					235					240	
35	CGG	AAG	CAG	CAG	ACC	ATC	ATC	CTG	GAT	GAC	GAG	CTG	ATC	CAG	TGG	AAG	768
	Arg	Lys	Gln	Gln	Thr	Ile	Ile	Leu	Asp	Asp	Glu	Leu	Ile	Gln	Trp	Lys	
					245					250					255		
40	CGG	CGG	CAG	CAG	CTG	GCC	GGG	AAC	GGC	GGG	CCC	CCC	GAG	GGC	AGC	CTG	816
	Arg	Arg	Gln	Gln	Leu	Ala	Gly	Asn	Gly	Gly	Pro	Pro	Glu	Gly	Ser	Leu	
					260				265					270			
45	GAC	GTG	CTA	CAG	TCC	TGG	TGT	GAG	AAG	TTG	GCC	GAG	ATC	ATC	TGG	CAG	864
	Asp	Val	Leu	Gln	Ser	Trp	Cys	Glu	Lys	Leu	Ala	Glu	Ile	Ile	Trp	Gln	
			275					280					285				
50	AAC	CGG	CAG	CAG	ATC	CGC	AGG	GCT	GAG	CAC	CTC	TGC	CAG	CAG	CTG	CCC	912
	Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu	Cys	Gln	Gln	Leu	Pro	
			290				295					300					
55	ATC	CCC	GGC	CCA	GTG	GAG	GAG	ATG	CTG	GCC	GAG	GTC	AAC	GCC	ACC	ATC	960
	Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu	Val	Asn	Ala	Thr	Ile	
	305					310					315					320	
60	ACG	GAC	ATT	ATC	TCA	GCC	CTG	GTG	ACC	AGC	ACA	TTC	ATC	ATT	GAG	AAG	1008
	Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	Phe	Ile	Ile	Glu	Lys	
					325					330					335		
65	CAG	CCT	CCT	CAG	GTC	CTG	AAG	ACC	CAG	ACC	AAG	TTT	GCA	GCC	ACC	GTA	1056
	Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	Phe	Ala	Ala	Thr	Val	
					340				345					350			
70	CGC	CTG	CTG	GTG	GGC	GGG	AAG	CTG	AAC	GTG	CAC	ATG	AAT	CCC	CCC	CAG	1104

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	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	Met	Asn	Pro	Pro	Gln	
			355					360					365				
5	GTG	AAG	GCC	ACC	ATC	ATC	AGT	GAG	CAG	CAG	GCC	AAG	TCT	CTG	CTT	AAA	1152
	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	Lys	Ser	Leu	Leu	Lys	
		370					375					380					
10	AAT	GAG	AAC	ACC	CGC	AAC	GAG	TGC	AGT	GGT	GAG	ATC	CTG	AAC	AAC	TGC	1200
	Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	Ile	Leu	Asn	Asn	Cys	
	385					390					395					400	
15	TGC	GTG	ATG	GAG	TAC	CAC	CAA	GCC	ACG	GGC	ACC	CTC	AGT	GCC	CAC	TTC	1248
	Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	Leu	Ser	Ala	His	Phe	
					405					410					415		
	AGG	AAC	ATG	TCA	CTG	AAG	AGG	ATC	AAG	CGT	GCT	GAC	CGG	CGG	GGT	GCA	1296
	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	Asp	Arg	Arg	Gly	Ala	
				420					425						430		
20	GAG	TCC	GTG	ACA	GAG	GAG	AAG	TTC	ACA	GTC	CTG	TTT	GAG	TCT	CAG	TTC	1344
	Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	Phe	Glu	Ser	Gln	Phe	
			435					440					445				
25	AGT	GTT	GGC	AGC	AAT	GAG	CTT	GTG	TTC	CAG	GTG	AAG	ACT	CTG	TCC	CTA	1392
	Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	Lys	Thr	Leu	Ser	Leu	
		450					455					460					
30	CCT	GTG	GTT	GTC	ATC	GTC	CAC	GGC	AGC	CAG	GAC	CAC	AAT	GCC	ACG	GCT	1440
	Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	His	Asn	Ala	Thr	Ala	
	465					470					475					480	
35	ACT	GTG	CTG	TGG	GAC	AAT	GCC	TTT	GCT	GAG	CCG	GGC	AGG	GTG	CCA	TTT	1488
	Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	Gly	Arg	Val	Pro	Phe	
					485					490					495		
	GCC	GTG	CCT	GAC	AAA	GTG	CTG	TGG	CCG	CAG	CTG	TGT	GAG	GCG	CTC	AAC	1536
	Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	Cys	Glu	Ala	Leu	Asn	
				500					505					510			
40	ATG	AAA	TTC	AAG	GCC	GAA	GTG	CAG	AGC	AAC	CGG	GGC	CTG	ACC	AAG	GAG	1584
	Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	Gly	Leu	Thr	Lys	Glu	
			515					520					525				
45	AAC	CTC	GTG	TTC	CTG	GCG	CAG	AAA	CTG	TTC	AAC	AAC	AGC	AGC	AGC	CAC	1632
	Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	Asn	Ser	Ser	Ser	His	
		530					535					540					
50	CTG	GAG	GAC	TAC	AGT	GGC	CTG	TCC	GTG	TCC	TGG	TCC	CAG	TTC	AAC	AGG	1680
	Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser	Trp	Ser	Gln	Phe	Asn	Arg	
	545					550					555					560	
55	GAG	AAC	TTG	CCG	GGC	TGG	AAC	TAC	ACC	TTC	TGG	CAG	TGG	TTT	GAC	GGG	1728
	Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	Gln	Trp	Phe	Asp	Gly	
					565					570					575		
	GTG	ATG	GAG	GTG	TTG	AAG	AAG	CAC	CAC	AAG	CCC	CAC	TGG	AAT	GAT	GGG	1776

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	Val	Met	Glu	Val	Leu	Lys	Lys	His	His	Lys	Pro	His	Trp	Asn	Asp	Gly	
				580					585					590			
5	GCC	ATC	CTA	GGT	TTT	GTG	AAT	AAG	CAA	CAG	GCC	CAC	GAC	CTG	CTC	ATC	1824
	Ala	Ile	Leu	Gly	Phe	Val	Asn	Lys	Gln	Gln	Ala	His	Asp	Leu	Leu	Ile	
			595					600					605				
10	AAC	AAG	CCC	GAC	GGG	ACC	TTC	TTG	TTG	CGC	TTT	AGT	GAC	TCA	GAA	ATC	1872
	Asn	Lys	Pro	Asp	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Asp	Ser	Glu	Ile	
		610					615					620					
15	GGG	GGC	ATC	ACC	ATC	GCC	TGG	AAG	TTT	GAC	TCC	CCG	GAA	CGC	AAC	CTG	1920
	Gly	Gly	Ile	Thr	Ile	Ala	Trp	Lys	Phe	Asp	Ser	Pro	Glu	Arg	Asn	Leu	
	625					630				635					640		
	TGG	AAC	CTG	AAA	CCA	TTC	ACC	ACG	CGG	GAT	TTC	TCC	ATC	AGG	TCC	CTG	1968
	Trp	Asn	Leu	Lys	Pro	Phe	Thr	Thr	Arg	Asp	Phe	Ser	Ile	Arg	Ser	Leu	
				645					650						655		
20	GCT	GAC	CGG	CTG	GGG	GAC	CTG	AGC	TAT	CTC	ATC	TAT	GTG	TTT	CCT	GAC	2016
	Ala	Asp	Arg	Leu	Gly	Asp	Leu	Ser	Tyr	Leu	Ile	Tyr	Val	Phe	Pro	Asp	
				660					665					670			
25	CGC	CCC	AAG	GAT	GAG	GTC	TTC	TCC	AAG	TAC	TAC	ACT	CCT	GTG	CTG	GCT	2064
	Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr	Tyr	Thr	Pro	Val	Leu	Ala	
			675					680					685				
30	AAA	GCT	GTT	GAT	GGA	TAT	GTG	AAA	CCA	CAG	ATC	AAG	CAA	GTG	GTC	CCT	2112
	Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln	Ile	Lys	Gln	Val	Val	Pro	
		690					695					700					
35	GAG	TTT	GTG	AAT	GCA	TCT	GCA	GAT	GCT	GGG	GGC	AGC	AGC	GCC	ACG	TAC	2160
	Glu	Phe	Val	Asn	Ala	Ser	Ala	Asp	Ala	Gly	Gly	Ser	Ser	Ala	Thr	Tyr	
	705					710				715					720		
	ATG	GAC	CAG	GCC	CCC	TCC	CCA	GCT	GTG	TGC	CCC	CAG	GCT	CCC	TAT	AAC	2208
	Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys	Pro	Gln	Ala	Pro	Tyr	Asn	
				725					730						735		
40	ATG	TAC	CCA	CAG	AAC	CCT	GAC	CAT	GTA	CTC	GAT	CAG	GAT	GGA	GAA	TTC	2256
	Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu	Asp	Gln	Asp	Gly	Glu	Phe	
				740				745						750			
45	GAC	CTG	GAT	GAG	ACC	ATG	GAT	GTG	GCC	AGG	CAC	GTG	GAG	GAA	CTC	TTA	2304
	Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg	His	Val	Glu	Glu	Leu	Leu	
			755					760					765				
50	CGC	CGA	CCA	ATG	GAC	AGT	CTT	GAC	TCC	CGC	CTC	TCG	CCC	CCT	GCC	GGT	2352
	Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg	Leu	Ser	Pro	Pro	Ala	Gly	
		770					775					780					
55	CTT	TTC	ACC	TCT	GCC	AGA	GGC	TCC	CTC	TCA	TGG	GTA	CCG	CGG	GCC	CGG	2400
	Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu	Ser	Trp	Val	Pro	Arg	Ala	Arg	
	785					790				795					800		
	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	2448

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	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	
					805					810					815		
5	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	2496
	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	
				820					825					830			
10	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	2544
	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	
			835					840					845				
15	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	2592
	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	
		850					855					860					
20	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	2640
	Pro	Thr	Leu	Val	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg		
	865					870				875					880		
25	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	2688
	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	
					885				890						895		
30	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	2736
	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	
				900					905					910			
35	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	2784
	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	
			915					920					925				
40	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	2832
	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	
		930					935					940					
45	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	2880
	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	
	945					950				955					960		
50	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	2928
	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	
					965				970					975			
55	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	2976
	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	
				980					985					990			
60	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	3024
	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	
			995					1000					1005				
65	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	3072
	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	
		1010						1015				1020					
70	ATG	GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	3120

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183

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
 1025 1030 1035 1040

5 GAC GAG CTG TAC AAG TAA 3138
 Asp Glu Leu Tyr Lys
 1045

(2) INFORMATION FOR SEQ ID NO:79:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1045 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln Gly Asp Ala Leu Arg
 1 5 10 15
 Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His
 20 25 30
 Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu
 35 40 45
 Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu
 50 55 60
 Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly
 65 70 75 80
 Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys
 85 90 95
 Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile
 100 105 110
 Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser
 115 120 125
 Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile
 130 135 140
 Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn
 145 150 155 160
 Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr
 165 170 175
 Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu
 180 185 190
 Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Gln Lys Gln
 195 200 205
 Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln
 210 215 220
 Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu
 225 230 235 240
 Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys
 245 250 255
 Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro Pro Glu Gly Ser Leu
 260 265 270
 Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln

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		275				280			285							
	Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu	Cys	Gln	Gln	Leu	Pro
		290					295					300				
5	Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu	Val	Asn	Ala	Thr	Ile
	305					310					315				320	
	Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	Phe	Ile	Ile	Glu	Lys
					325					330					335	
	Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	Phe	Ala	Ala	Thr	Val
				340					345					350		
10	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	Met	Asn	Pro	Pro	Gln
				355				360					365			
	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	Lys	Ser	Leu	Leu	Lys
	370						375					380				
15	Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	Ile	Leu	Asn	Asn	Cys
	385					390					395				400	
	Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	Leu	Ser	Ala	His	Phe
					405					410					415	
	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	Asp	Arg	Arg	Gly	Ala
				420					425					430		
20	Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	Phe	Glu	Ser	Gln	Phe
				435				440					445			
	Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	Lys	Thr	Leu	Ser	Leu
	450					455						460				
25	Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	His	Asn	Ala	Thr	Ala
	465					470					475				480	
	Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	Gly	Arg	Val	Pro	Phe
					485					490					495	
	Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	Cys	Glu	Ala	Leu	Asn
				500					505					510		
30	Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	Gly	Leu	Thr	Lys	Glu
				515				520					525			
	Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	Asn	Ser	Ser	Ser	His
	530					535					540					
35	Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser	Trp	Ser	Gln	Phe	Asn	Arg
	545					550					555				560	
	Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	Gln	Trp	Phe	Asp	Gly
					565				570					575		
	Val	Met	Glu	Val	Leu	Lys	Lys	His	His	Lys	Pro	His	Trp	Asn	Asp	Gly
				580				585					590			
40	Ala	Ile	Leu	Gly	Phe	Val	Asn	Lys	Gln	Gln	Ala	His	Asp	Leu	Leu	Ile
				595				600					605			
	Asn	Lys	Pro	Asp	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Asp	Ser	Glu	Ile
	610					615					620					
	Gly	Gly	Ile	Thr	Ile	Ala	Trp	Lys	Phe	Asp	Ser	Pro	Glu	Arg	Asn	Leu
45	625					630					635				640	
	Trp	Asn	Leu	Lys	Pro	Phe	Thr	Thr	Arg	Asp	Phe	Ser	Ile	Arg	Ser	Leu
					645					650					655	
	Ala	Asp	Arg	Leu	Gly	Asp	Leu	Ser	Tyr	Leu	Ile	Tyr	Val	Phe	Pro	Asp
				660				665					670			
50	Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr	Tyr	Thr	Pro	Val	Leu	Ala
				675				680					685			
	Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln	Ile	Lys	Gln	Val	Val	Pro
	690					695						700				
	Glu	Phe	Val	Asn	Ala	Ser	Ala	Asp	Ala	Gly	Gly	Ser	Ser	Ala	Thr	Tyr
55	705					710					715				720	
	Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys	Pro	Gln	Ala	Pro	Tyr	Asn

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				725					730					735
	Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu	Asp	Gln	Asp	Gly
				740					745					750
5	Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg	His	Val	Glu	Glu
			755					760					765	
	Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg	Leu	Ser	Pro	Pro
			770				775					780		
	Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu	Ser	Trp	Val	Pro	Arg
	785					790					795			800
10	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu
				805						810				815
	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn
				820					825				830	
15	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr
			835						840				845	
	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val
	850						855					860		
	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe
	865					870				875				880
20	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala
				885						890				895
	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp
			900						905				910	
25	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu
			915					920					925	
	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn
	930					935						940		
	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr
	945				950					955				960
30	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile
				965						970				975
	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln
			980						985				990	
35	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His
			995				1000					1005		
	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg
	1010					1015					1020			
	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu
	025				1030					1035				1040
40	Asp	Glu	Leu	Tyr	Lys									
					1045									

(2) INFORMATION FOR SEQ ID NO:80:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TGGGATCCTC AGGCCGTGCT GCTGGCCG

28

55

(2) INFORMATION FOR SEQ ID NO:81:

185

186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTCTCGAGGG AGCATGGGCA CCTTGCG

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGGATCCGA GAAGTCTATA TCCCATC

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGGGATCCTT AGAAGTCTAT ATCCCATC

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTCTCGAGCC ATGAACGCCC CCGAGCGG

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

187

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGAATTCTC GTCTGATTTT TGGCAGGAGG

30

(2) INFORMATION FOR SEQ ID NO:86:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

20 GTGAATTCTT TACGTCTGAT TTCTGGCAGG

30

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCTCGAGCC ATGGACGAAC TGTTCCCCCT CATC

34

35 (2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

45

GTGGATCCAA GGAGCTGATC TGA CTCAGCA G

31

(2) INFORMATION FOR SEQ ID NO:89:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

187

188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGATCCTT AGGAGCTGAT CTGACTCAGC AG

32

5 (2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

15

CCTCCTAAGC TTATCATGGA CCATTATGAT TC

32

(2) INFORMATION FOR SEQ ID NO:91:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

30

CCTCCTGGAT CCCTGCGCAG GATGATGGTC CAG

33

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGATGGAAGC TTCAATGGCT GCCATCCGGA AGAAACTGGT GATTG

45

(2) INFORMATION FOR SEQ ID NO:93:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

55

GGATGGGGAT CCTCACAAGA CAAGGCAACC AGATTTTTTC TTCCC

45

188

189

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGGAAGCTTC CATGAGCGAG ACGGTCATC

29

(2) INFORMATION FOR SEQ ID NO:95:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

25 CCCGGATCCT CAGGGAGAAC CCCGCTTC

28

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTGAATTCTGA CCATGGAGCG GCCCCCGGGG

30

40 (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

50

GTGGTACCCA TTCTGTTAAC CAACTCC

27

(2) INFORMATION FOR SEQ ID NO:98:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

189

190

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGGTACCTC ATTCTGTAA CCAACTCC

28

10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

20

GTCTCGAGAG ATGCTGTCCC GTGGGTGG

28

(2) INFORMATION FOR SEQ ID NO:100:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGAATTCGC TTCCTCTTGA GGGAACC

27

35

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTGAATTCAC TTCCTCTTGA GGGAACC

27

45

(2) INFORMATION FOR SEQ ID NO:102:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTCTCGAGCC ATGGAGAACT TCCAAAAGG

29

5

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGGATCCCA GAGTCGAAGA TGGGGTAC

28

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

30 GTGGATCCTC AGAGTCGAAG ATGGGGTAC

29

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGAATTCGG CGATGCCAGA CCCC GCGGCG

30

45

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

55

GTGGATCCCA GGCACAGGCA GCCTCAGCCT TC

32

191

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTGGATCCTC AGGCACAGGC AGCCTCAGCC TTC

33

15

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 2616 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2613
 (D) OTHER INFORMATION:

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

35

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

40

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

45

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

50

CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

55

CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG 336

192

193

	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
5	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
10	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					
15	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150				155						160	
20	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
25	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185						190			
30	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
35	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
40	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
45	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCG	AAT	TCG	GCG	ATG	CCA	GAC	CCC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Met	Pro	Asp	Pro	
					245				250						255		
50	GCG	GCG	CAC	CTG	CCC	TTC	TTC	TAC	GGC	AGC	ATC	TCG	CGT	GCC	GAG	GCC	816
	Ala	Ala	His	Leu	Pro	Phe	Phe	Tyr	Gly	Ser	Ile	Ser	Arg	Ala	Glu	Ala	
				260					265					270			
55	GAG	GAG	CAC	CTG	AAG	CTG	GCG	GGC	ATG	GCG	GAC	GGG	CTC	TTC	CTG	CTG	864
	Glu	Glu	His	Leu	Lys	Leu	Ala	Gly	Met	Ala	Asp	Gly	Leu	Phe	Leu	Leu	
			275				280						285				
60	CGC	CAG	TGC	CTG	CGC	TCG	CTG	GGC	GGC	TAT	GTG	CTG	TCG	CTC	GTG	CAC	912
	Arg	Gln	Cys	Leu	Arg	Ser	Leu	Gly	Gly	Tyr	Val	Leu	Ser	Leu	Val	His	
		290					295					300					
65	GAT	GTG	CGC	TTC	CAC	CAC	TTT	CCC	ATC	GAG	CGC	CAG	CTC	AAC	GGC	ACC	960
	Asp	Val	Arg	Phe	His	His	Phe	Pro	Ile	Glu	Arg	Gln	Leu	Asn	Gly	Thr	
	305					310					315					320	
70	TAC	GCC	ATT	GCC	GGC	GGC	AAA	GCG	CAC	TGT	GGA	CCG	GCA	GAG	CTC	TGC	1008

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194

	Tyr	Ala	Ile	Ala	Gly	Gly	Lys	Ala	His	Cys	Gly	Pro	Ala	Glu	Leu	Cys	
					325					330					335		
5	GAG	TTC	TAC	TCG	CGC	GAC	CCC	GAC	GGG	CTG	CCC	TGC	AAC	CTG	CGC	AAG	1056
	Glu	Phe	Tyr	Ser	Arg	Asp	Pro	Asp	Gly	Leu	Pro	Cys	Asn	Leu	Arg	Lys	
				340					345					350			
10	CCG	TGC	AAC	CGG	CCG	TCG	GGC	CTC	GAG	CCG	CAG	CCG	GGG	GTC	TTC	GAC	1104
	Pro	Cys	Asn	Arg	Pro	Ser	Gly	Leu	Glu	Pro	Gln	Pro	Gly	Val	Phe	Asp	
				355				360					365				
15	TGC	CTG	CGA	GAC	GCC	ATG	GTG	CGT	GAC	TAC	GTG	CGC	CAG	ACG	TGG	AAG	1152
	Cys	Leu	Arg	Asp	Ala	Met	Val	Arg	Asp	Tyr	Val	Arg	Gln	Thr	Trp	Lys	
		370					375					380					
20	CTG	GAG	GGC	GAG	GCC	CTG	GAG	CAG	GCC	ATC	ATC	AGC	CAG	GCC	CCG	CAG	1200
	Leu	Glu	Gly	Glu	Ala	Leu	Glu	Gln	Ala	Ile	Ile	Ser	Gln	Ala	Pro	Gln	
	385					390				395					400		
25	GTG	GAG	AAG	CTC	ATT	GCT	ACG	ACG	GCC	CAC	GAG	CGG	ATG	CCC	TGG	TAC	1248
	Val	Glu	Lys	Leu	Ile	Ala	Thr	Thr	Ala	His	Glu	Arg	Met	Pro	Trp	Tyr	
				405					410						415		
30	CAC	AGC	AGC	CTG	ACG	CGT	GAG	GAG	GCC	GAG	CGC	AAA	CTT	TAC	TCT	GGG	1296
	His	Ser	Ser	Leu	Thr	Arg	Glu	Glu	Ala	Glu	Arg	Lys	Leu	Tyr	Ser	Gly	
				420					425					430			
35	GCG	CAG	ACC	GAC	GGC	AAG	TTC	CTG	CTG	AGG	CCG	CGG	AAG	GAG	CAG	GGC	1344
	Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	Arg	Pro	Arg	Lys	Glu	Gln	Gly	
			435					440					445				
40	ACA	TAC	GCC	CTG	TCC	CTC	ATC	TAT	GGG	AAG	ACG	GTG	TAC	CAC	TAC	CTC	1392
	Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	Lys	Thr	Val	Tyr	His	Tyr	Leu	
		450					455					460					
45	ATC	AGC	CAA	GAC	AAG	GCG	GGC	AAG	TAC	TGC	ATT	CCC	GAG	GGC	ACC	AAG	1440
	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro	Glu	Gly	Thr	Lys	
	465				470				475					480			
50	TTT	GAC	ACG	CTC	TGG	CAG	CTG	GTG	GAG	TAT	CTG	AAG	CTG	AAG	GCG	GAC	1488
	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys	Leu	Lys	Ala	Asp	
				485				490						495			
55	GGG	CTC	ATC	TAC	TGC	CTG	AAG	GAG	GCC	TGC	CCC	AAC	AGC	AGT	GCC	AGC	1536
	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	Asn	Ser	Ser	Ala	Ser	
			500					505					510				
60	AAC	GCC	TCA	GGG	GCT	GCT	GCT	CCC	ACA	CTC	CCA	GCC	CAC	CCA	TCC	ACG	1584
	Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala	His	Pro	Ser	Thr	
			515					520					525				
65	TTG	ACT	CAT	CCT	CAG	AGA	CGA	ATC	GAC	ACC	CTC	AAC	TCA	GAT	GGA	TAC	1632
	Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn	Ser	Asp	Gly	Tyr	
		530					535					540					
70	ACC	CCT	GAG	CCA	GCA	CGC	ATA	ACG	TCC	CCA	GAC	AAA	CCG	CGG	CCG	ATG	1680

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195

	Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys	Pro	Arg	Pro	Met	
	545					550					555					560	
5	CCC	ATG	GAC	ACG	AGC	GTG	TAT	GAG	AGC	CCC	TAC	AGC	GAC	CCA	GAG	GAG	1728
	Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser	Asp	Pro	Glu	Glu	
					565					570					575		
10	CTC	AAG	GAC	AAG	AAG	CTC	TTC	CTG	AAG	CGC	GAT	AAC	CTC	CTC	ATA	GCT	1776
	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Lys	Arg	Asp	Asn	Leu	Leu	Ile	Ala	
				580					585					590			
15	GAC	ATT	GAA	CTT	GGC	TGC	GGC	AAC	TTT	GGC	TCA	GTG	CGC	CAG	GGC	GTG	1824
	Asp	Ile	Glu	Leu	Gly	Cys	Gly	Asn	Phe	Gly	Ser	Val	Arg	Gln	Gly	Val	
			595				600						605				
20	TAC	CGC	ATG	CGC	AAG	AAG	CAG	ATC	GAC	GTG	GCC	ATC	AAG	GTG	CTG	AAG	1872
	Tyr	Arg	Met	Arg	Lys	Lys	Gln	Ile	Asp	Val	Ala	Ile	Lys	Val	Leu	Lys	
	610						615					620					
25	CAG	GGC	ACG	GAG	AAG	GCA	GAC	ACG	GAA	GAG	ATG	ATG	CGC	GAG	GCG	CAG	1920
	Gln	Gly	Thr	Glu	Lys	Ala	Asp	Thr	Glu	Glu	Met	Met	Arg	Glu	Ala	Gln	
	625					630					635					640	
30	ATC	ATG	CAC	CAG	CTG	GAC	AAC	CCC	TAC	ATC	GTG	CGG	CTC	ATT	GGC	GTC	1968
	Ile	Met	His	Gln	Leu	Asp	Asn	Pro	Tyr	Ile	Val	Arg	Leu	Ile	Gly	Val	
				645						650					655		
35	TGC	CAG	GCC	GAG	GCC	CTC	ATG	CTG	GTC	ATG	GAG	ATG	GCT	GGG	GGC	GGG	2016
	Cys	Gln	Ala	Glu	Ala	Leu	Met	Leu	Val	Met	Glu	Met	Ala	Gly	Gly	Gly	
				660					665					670			
40	CCG	CTG	CAC	AAG	TTC	CTG	GTC	GGC	AAG	AGG	GAG	GAG	ATC	CCT	GTG	AGC	2064
	Pro	Leu	His	Lys	Phe	Leu	Val	Gly	Lys	Arg	Glu	Glu	Ile	Pro	Val	Ser	
			675					680					685				
45	AAT	GTG	GCC	GAG	CTG	CTG	CAC	CAG	GTG	TCC	ATG	GGG	ATG	AAG	TAC	CTG	2112
	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met	Gly	Met	Lys	Tyr	Leu	
	690						695					700					
50	GAG	GAG	AAG	AAC	TTT	GTG	CAC	CGT	GAC	CTG	GCG	GCC	CGC	AAC	GTC	CTG	2160
	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	
	705					710					715				720		
55	CTG	GTT	AAC	CGG	CAC	TAC	GCC	AAG	ATC	AGC	GAC	TTT	GGC	CTC	TCC	AAA	2208
	Leu	Val	Asn	Arg	His	Tyr	Ala	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ser	Lys	
				725						730					735		
60	GCA	CTG	GGT	GCC	GAC	GAC	AGC	TAC	TAC	ACT	GCC	CGC	TCA	GCA	GGG	AAG	2256
	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala	Arg	Ser	Ala	Gly	Lys	
				740					745					750			
65	TGG	CCG	CTC	AAG	TGG	TAC	GCA	CCC	GAA	TGC	ATC	AAC	TTC	CGC	AAG	TTC	2304
	Trp	Pro	Leu	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile	Asn	Phe	Arg	Lys	Phe	
			755					760						765			
70	TCC	AGC	CGC	AGC	GAT	GTC	TGG	AGC	TAT	GGG	GTC	ACC	ATG	TGG	GAG	GCC	2352

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	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Met	Trp	Glu	Ala	
	770						775					780					
5	TTG	TCC	TAC	GGC	CAG	AAG	CCC	TAC	AAG	AAG	ATG	AAA	GGG	CCG	GAG	GTC	2400
	Leu	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Lys	Lys	Met	Lys	Gly	Pro	Glu	Val	
	785					790				795					800		
10	ATG	GCC	TTC	ATC	GAG	CAG	GGC	AAG	CGG	ATG	GAG	TGC	CCA	CCA	GAG	TGT	2448
	Met	Ala	Phe	Ile	Glu	Gln	Gly	Lys	Arg	Met	Glu	Cys	Pro	Pro	Glu	Cys	
				805					810						815		
15	CCA	CCC	GAA	CTG	TAC	GCA	CTC	ATG	AGT	GAC	TGC	TGG	ATC	TAC	AAG	TGG	2496
	Pro	Pro	Glu	Leu	Tyr	Ala	Leu	Met	Ser	Asp	Cys	Trp	Ile	Tyr	Lys	Trp	
				820				825					830				
	GAG	GAT	CGC	CCC	GAC	TTC	CTG	ACC	GTG	GAG	CAG	CGC	ATG	CGA	GCC	TGT	2544
	Glu	Asp	Arg	Pro	Asp	Phe	Leu	Thr	Val	Glu	Gln	Arg	Met	Arg	Ala	Cys	
			835					840				845					
20	TAC	TAC	AGC	CTG	GCC	AGC	AAG	GTG	GAA	GGG	CCC	CCA	GGC	AGC	ACA	CAG	2592
	Tyr	Tyr	Ser	Leu	Ala	Ser	Lys	Val	Glu	Gly	Pro	Pro	Gly	Ser	Thr	Gln	
		850					855					860					
25	AAG	GCT	GAG	GCT	GCC	TGT	GCC	TGA									2616
	Lys	Ala	Glu	Ala	Ala	Cys	Ala										
	865					870											

(2) INFORMATION FOR SEQ ID NO:109:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 871 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
45	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30				
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45					
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60							
50	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75					80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85				90					95				
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
55			100				105				110						
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	

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		115		120		125													
		Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
		130						135					140						
5		Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
		145					150					155				160			
		Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
						165				170					175				
		Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
					180					185				190					
10		Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu		
					195				200					205					
		Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe		
					210				215				220						
15		Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser		
		225					230					235				240			
		Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Met	Pro	Asp	Pro		
						245					250				255				
		Ala	Ala	His	Leu	Pro	Phe	Phe	Tyr	Gly	Ser	Ile	Ser	Arg	Ala	Glu	Ala		
					260					265				270					
20		Glu	Glu	His	Leu	Lys	Leu	Ala	Gly	Met	Ala	Asp	Gly	Leu	Phe	Leu	Leu		
				275					280					285					
		Arg	Gln	Cys	Leu	Arg	Ser	Leu	Gly	Gly	Tyr	Val	Leu	Ser	Leu	Val	His		
				290					295				300						
		Asp	Val	Arg	Phe	His	His	Phe	Pro	Ile	Glu	Arg	Gln	Leu	Asn	Gly	Thr		
25		305					310					315				320			
		Tyr	Ala	Ile	Ala	Gly	Gly	Lys	Ala	His	Cys	Gly	Pro	Ala	Glu	Leu	Cys		
						325					330				335				
		Glu	Phe	Tyr	Ser	Arg	Asp	Pro	Asp	Gly	Leu	Pro	Cys	Asn	Leu	Arg	Lys		
					340					345				350					
30		Pro	Cys	Asn	Arg	Pro	Ser	Gly	Leu	Glu	Pro	Gln	Pro	Gly	Val	Phe	Asp		
					355				360					365					
		Cys	Leu	Arg	Asp	Ala	Met	Val	Arg	Asp	Tyr	Val	Arg	Gln	Thr	Trp	Lys		
				370					375				380						
		Leu	Glu	Gly	Glu	Ala	Leu	Glu	Gln	Ala	Ile	Ile	Ser	Gln	Ala	Pro	Gln		
35		385					390					395				400			
		Val	Glu	Lys	Leu	Ile	Ala	Thr	Thr	Ala	His	Glu	Arg	Met	Pro	Trp	Tyr		
						405					410				415				
		His	Ser	Ser	Leu	Thr	Arg	Glu	Glu	Ala	Glu	Arg	Lys	Leu	Tyr	Ser	Gly		
					420					425				430					
40		Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	Arg	Pro	Arg	Lys	Glu	Gln	Gly		
					435					440				445					
		Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	Lys	Thr	Val	Tyr	His	Tyr	Leu		
					450				455				460						
		Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro	Glu	Gly	Thr	Lys		
45		465					470					475				480			
		Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys	Leu	Lys	Ala	Asp		
						485					490				495				
		Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	Asn	Ser	Ser	Ala	Ser		
					500					505				510					
50		Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala	His	Pro	Ser	Thr		
					515					520				525					
		Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn	Ser	Asp	Gly	Tyr		
					530				535				540						
		Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys	Pro	Arg	Pro	Met		
55		545					550					555				560			
		Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser	Asp	Pro	Glu	Glu		

197

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565 570 575
 Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala
 580 585 590
 Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val
 595 600 605
 Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys
 610 615 620
 Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln
 625 630 635 640
 10 Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val
 645 650 655
 Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly
 660 665 670
 Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser
 675 680 685
 15 Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu
 690 695 700
 Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu
 705 710 715 720
 20 Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys
 725 730 735
 Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys
 740 745 750
 Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe
 755 760 765
 25 Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala
 770 775 780
 Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val
 785 790 795 800
 30 Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys
 805 810 815
 Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp
 820 825 830
 Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys
 835 840 845
 35 Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln
 850 855 860
 Lys Ala Glu Ala Ala Cys Ala
 865 870
 40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2595
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

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	ATG CCA GAC CCC GCG GCG CAC CTG CCC TTC TTC TAC GGC AGC ATC TCG	48
	Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser	
	1 5 10 15	
5	CGT GCC GAG GCC GAG GAG CAC CTG AAG CTG GCG GGC ATG GCG GAC GGG	96
	Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly	
	20 25 30	
10	CTC TTC CTG CTG CGC CAG TGC CTG CGC TCG CTG GGC GGC TAT GTG CTG	144
	Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu	
	35 40 45	
15	TCG CTC GTG CAC GAT GTG CGC TTC CAC CAC TTT CCC ATC GAG CGC CAG	192
	Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln	
	50 55 60	
20	CTC AAC GGC ACC TAC GCC ATT GCC GGC GGC AAA GCG CAC TGT GGA CCG	240
	Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro	
	65 70 75 80	
25	GCA GAG CTC TGC GAG TTC TAC TCG CGC GAC CCC GAC GGC CTG CCC TGC	288
	Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys	
	85 90 95	
30	AAC CTG CGC AAG CCG TGC AAC CGG CCG TCG GGC CTC GAG CCG CAG CCG	336
	Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro	
	100 105 110	
35	GGG GTC TTC GAC TGC CTG CGA GAC GCC ATG GTG CGT GAC TAC GTG CGC	384
	Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg	
	115 120 125	
40	CAG ACG TGG AAG CTG GAG GGC GAG GCC CTG GAG CAG GCC ATC ATC AGC	432
	Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser	
	130 135 140	
45	CAG GCC CCG CAG GTG GAG AAG CTC ATT GCT ACG ACG GCC CAC GAG CGG	480
	Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg	
	145 150 155 160	
50	ATG CCC TGG TAC CAC AGC AGC CTG ACG CGT GAG GAG GCC GAG CGC AAA	528
	Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys	
	165 170 175	
55	CTT TAC TCT GGG GCG CAG ACC GAC GGC AAG TTC CTG CTG AGG CCG CGG	576
	Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg	
	180 185 190	
60	AAG GAG CAG GGC ACA TAC GCC CTG TCC CTC ATC TAT GGG AAG ACG GTG	624
	Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val	
	195 200 205	
65	TAC CAC TAC CTC ATC AGC CAA GAC AAG GCG GGC AAG TAC TGC ATT CCC	672
	Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro	
	210 215 220	

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200

5	GAG GGC ACC AAG TTT GAC ACG CTC TGG CAG CTG GTG GAG TAT CTG AAG	720
	Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys	
	225 230 235 240	
	CTG AAG GCG GAC GGG CTC ATC TAC TGC CTG AAG GAG GCC TGC CCC AAC	768
	Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn	
10	245 250 255	
	AGC AGT GCC AGC AAC GCC TCA GGG GCT GCT GCT CCC ACA CTC CCA GCC	816
	Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala	
	260 265 270	
	CAC CCA TCC ACG TTG ACT CAT CCT CAG AGA CGA ATC GAC ACC CTC AAC	864
15	His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn	
	275 280 285	
	TCA GAT GGA TAC ACC CCT GAG CCA GCA CGC ATA ACG TCC CCA GAC AAA	912
	Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys	
	290 295 300	
20	CCG CGG CCG ATG CCC ATG GAC ACG AGC GTG TAT GAG AGC CCC TAC AGC	960
	Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser	
	305 310 315 320	
	GAC CCA GAG GAG CTC AAG GAC AAG AAG CTC TTC CTG AAG CGC GAT AAC	1008
	Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn	
25	325 330 335	
	CTC CTC ATA GCT GAC ATT GAA CTT GGC TGC GGC AAC TTT GGC TCA GTG	1056
	Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val	
	340 345 350	
	CGC CAG GGC GTG TAC CGC ATG CGC AAG AAG CAG ATC GAC GTG GCC ATC	1104
30	Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile	
	355 360 365	
	AAG GTG CTG AAG CAG GGC ACG GAG AAG GCA GAC ACG GAA GAG ATG ATG	1152
	Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met	
	370 375 380	
35	CGC GAG GCG CAG ATC ATG CAC CAG CTG GAC AAC CCC TAC ATC GTG CGG	1200
	Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg	
	385 390 395 400	
	CTC ATT GGC GTC TGC CAG GCC GAG GCC CTC ATG CTG GTC ATG GAG ATG	1248
	Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met	
40	405 410 415	
	GCT GGG GGC GGG CCG CTG CAC AAG TTC CTG GTC GGC AAG AGG GAG GAG	1296
	Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu	
	420 425 430	
	ATC CCT GTG AGC AAT GTG GCC GAG CTG CTG CAC CAG GTG TCC ATG GGG	1344
45	Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly	
	435 440 445	
50		
55		

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5	ATG AAG TAC CTG GAG GAG AAG AAC TTT GTG CAC CGT GAC CTG GCG GCC	1392
	Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala	
	450 455 460	
	CGC AAC GTC CTG CTG GTT AAC CGG CAC TAC GCC AAG ATC AGC GAC TTT	1440
	Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe	
10	465 470 475 480	
	GGC CTC TCC AAA GCA CTG GGT GCC GAC GAC AGC TAC TAC ACT GCC CGC	1488
	Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg	
	485 490 495	
	TCA GCA GGG AAG TGG CCG CTC AAG TGG TAC GCA CCC GAA TGC ATC AAC	1536
15	Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn	
	500 505 510	
	TTC CGC AAG TTC TCC AGC CGC AGC GAT GTG TGG AGC TAT GGG GTC ACC	1584
	Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr	
	515 520 525	
20	ATG TGG GAG GCC TTG TCC TAC GGC CAG AAG CCC TAC AAG AAG ATG AAA	1632
	Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys	
	530 535 540	
	GGG CCG GAG GTC ATG GCC TTC ATC GAG CAG GGC AAG CGG ATG GAG TGC	1680
	Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys	
25	545 550 555 560	
	CCA CCA GAG TGT CCA CCC GAA CTG TAC GCA CTC ATG AGT GAC TGC TGG	1728
	Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp	
	565 570 575	
	ATC TAC AAG TGG GAG GAT CGC CCC GAC TTC CTG ACC GTG GAG CAG CGC	1776
30	Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg	
	580 585 590	
	ATG CGA GCC TGT TAC TAC AGC CTG GCC AGC AAG GTG GAA GGG CCC CCA	1824
	Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro	
	595 600 605	
35	GGC AGC ACA CAG AAG GCT GAG GCT GCC TGT GCC TGG GAT CCA CCG GTC	1872
	Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala Trp Asp Pro Pro Val	
	610 615 620	
	GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC	1920
	Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro	
40	625 630 635 640	
	ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG	1968
	Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val	
	645 650 655	
	TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG	2016
45	Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	
	660 665 670	
50		
55		

201

[illegible]

202

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
 1 5 10 15
 Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
 15 20 25 30
 Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
 35 40 45
 Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
 50 55 60
 Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
 65 70 75 80
 Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
 85 90 95
 Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
 100 105 110
 Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
 115 120 125
 Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
 130 135 140
 Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
 145 150 155 160
 Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
 165 170 175
 Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
 180 185 190
 Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val
 195 200 205
 Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
 210 215 220
 Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
 225 230 235 240
 Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
 245 250 255
 Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
 260 265 270
 His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn
 275 280 285
 Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys
 290 295 300
 Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser
 305 310 315 320
 Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn
 325 330 335
 Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val
 340 345 350
 Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile

203

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		355				360				365						
		Lys	Val	Leu	Lys	Gln	Gly	Thr	Glu	Lys	Ala	Asp	Thr	Glu	Glu	Met
		370						375					380			Met
5		Arg	Glu	Ala	Gln	Ile	Met	His	Gln	Leu	Asp	Asn	Pro	Tyr	Ile	Val
		385					390					395				400
		Leu	Ile	Gly	Val	Cys	Gln	Ala	Glu	Ala	Leu	Met	Leu	Val	Met	Glu
						405					410					415
		Ala	Gly	Gly	Gly	Pro	Leu	His	Lys	Phe	Leu	Val	Gly	Lys	Arg	Glu
						420				425					430	Glu
10		Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met
						435			440					445		Gly
		Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala
		450						455					460			Ala
15		Arg	Asn	Val	Leu	Leu	Val	Asn	Arg	His	Tyr	Ala	Lys	Ile	Ser	Asp
		465					470						475			Phe
		Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala
						485					490					Arg
		Ser	Ala	Gly	Lys	Trp	Pro	Leu	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile
						500				505				510		Asn
20		Phe	Arg	Lys	Phe	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val
						515				520				525		Thr
		Met	Trp	Glu	Ala	Leu	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Lys	Lys	Met
		530						535					540			Lys
25		Gly	Pro	Glu	Val	Met	Ala	Phe	Ile	Glu	Gln	Gly	Lys	Arg	Met	Glu
		545					550					555				Cys
		Pro	Pro	Glu	Cys	Pro	Pro	Glu	Leu	Tyr	Ala	Leu	Met	Ser	Asp	Cys
						565					570					Trp
		Ile	Tyr	Lys	Trp	Glu	Asp	Arg	Pro	Asp	Phe	Leu	Thr	Val	Glu	Gln
						580				585					590	Arg
30		Met	Arg	Ala	Cys	Tyr	Tyr	Ser	Leu	Ala	Ser	Lys	Val	Glu	Gly	Pro
						595			600					605		Pro
		Gly	Ser	Thr	Gln	Lys	Ala	Glu	Ala	Ala	Cys	Ala	Trp	Asp	Pro	Pro
						610			615				620			Val
35		Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val
		625					630					635				Pro
		Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser
						645					650				655	Val
		Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu
						660				665				670		Lys
40		Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu
						675			680					685		Val
		Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp
						690			695				700			His
45		Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr
		705					710					715				Val
		Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr
						725					730					Arg
		Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu
						740				745					750	Leu
50		Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys
						755				760				765		Leu
		Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys
						770			775				780			Gln
55		Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu
		785					790					795				Asp
		Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile
																Gly

204

205

805 810 815
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 820 825 830
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 835 840 845
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 850 855 860
 Lys
 865

10

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1635 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1632
 (D) OTHER INFORMATION:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

30
 1 5 10 15
 ATG GAG AAC TTC CAA AAG GTG GAA AAG ATC GGA GAG GGC ACG TAC GGA
 Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 35
 20 25 30
 GTT GTG TAC AAA GCC AGA AAC AAG TTG ACG GGA GAG GTG GTG GCG CTT
 Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
 40
 35
 AAG AAA ATC CGC CTG GAC ACT GAG ACT GAG GGT GTG CCC AGT ACT GCC
 Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
 40
 50 55 60
 ATC CGA GAG ATC TCT CTG CTT AAG GAG CTT AAC CAT CCT AAT ATT GTC
 Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
 45
 65 70 75 80
 AAG CTG CTG GAT GTC ATT CAC ACA GAA AAT AAA CTC TAC CTG GTT TTT
 Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
 50
 85 90 95
 GAA TTT CTG CAC CAA GAT CTC AAG AAA TTC ATG GAT GCC TCT GCT CTC
 Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
 55
 100 105 110
 ACT GGC ATT CCT CTT CCC CTC ATC AAG AGC TAT CTG TTC CAG CTG CTC
 Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
 55
 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
 CAG GGC CTA GCT TTC TGC CAT TCT CAT CGG GTC CTC CAC CGA GAC CTT

205

206

	Gln	Gly	Leu	Ala	Phe	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	Asp	Leu	
			115					120					125				
5	AAA	CCT	CAG	AAT	CTG	CTT	ATT	AAC	ACA	GAG	GGG	GCC	ATC	AAG	CTA	GCA	432
	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Thr	Glu	Gly	Ala	Ile	Lys	Leu	Ala	
			130				135					140					
10	GAC	TTT	GGA	CTA	GCC	AGA	GCT	TTT	GGA	GTC	CCT	GTT	CGT	ACT	TAC	ACC	480
	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Val	Arg	Thr	Tyr	Thr	
			145			150					155					160	
15	CAT	GAG	GTG	GTG	ACC	CTG	TGG	TAC	CGA	GCT	CCT	GAA	ATC	CTC	CTG	GGC	528
	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly	
					165				170						175		
20	TCG	AAA	TAT	TAT	TCC	ACA	GCT	GTG	GAC	ATC	TGG	AGC	CTG	GGC	TGC	ATC	576
	Ser	Lys	Tyr	Tyr	Ser	Thr	Ala	Val	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Ile	
					180				185					190			
25	TTT	GCT	GAG	ATG	GTG	ACT	CGC	CGG	GCC	CTG	TTC	CCT	GGA	GAT	TCT	GAG	624
	Phe	Ala	Glu	Met	Val	Thr	Arg	Arg	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu	
				195				200					205				
30	ATT	GAC	CAG	CTC	TTC	CGG	ATC	TTT	CGG	ACT	CTG	GGG	ACC	CCA	GAT	GAG	672
	Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Thr	Leu	Gly	Thr	Pro	Asp	Glu	
			210				215					220					
35	GTG	GTG	TGG	CCA	GGA	GTT	ACT	TCT	ATG	CCT	GAT	TAC	AAG	CCA	AGT	TTC	720
	Val	Val	Trp	Pro	Gly	Val	Thr	Ser	Met	Pro	Asp	Tyr	Lys	Pro	Ser	Phe	
			225			230					235					240	
40	CCC	AAG	TGG	GCC	CGG	CAA	GAT	TTT	AGT	AAA	GTT	GTA	CCT	CCC	CTG	GAT	768
	Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys	Val	Val	Pro	Pro	Leu	Asp	
					245					250					255		
45	GAA	GAT	GGA	CGG	AGC	TTG	TTA	TCG	CAA	ATG	CTG	CAC	TAC	GAC	CCT	AAC	816
	Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met	Leu	His	Tyr	Asp	Pro	Asn	
				260					265				270				
50	AAG	CGG	ATT	TCG	GCC	AAG	GCA	GCC	CTG	GCT	CAC	CCT	TTC	TTC	CAG	GAT	864
	Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala	His	Pro	Phe	Phe	Gln	Asp	
				275				280					285				
55	GTG	ACC	AAG	CCA	GTA	CCC	CAT	CTT	CGA	CTC	TGG	GAT	CCA	CCG	GTC	GCC	912
	Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu	Trp	Asp	Pro	Pro	Val	Ala	
			290				295					300					
60	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	960
	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	
						310					315				320		
65	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	1008
	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	
					325					330					335		
70	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	1056

206

207

	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	
				340					345					350			
5	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	1104
	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	
			355					360					365				
10	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	1152
	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	
			370				375					380					
15	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	1200
	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	
	385					390					395					400	
20	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	1248
	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	
					405					410					415		
25	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	1296
	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	
				420					425					430			
30	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	1344
	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	
			435					440					445				
35	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	1392
	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	
			450				455					460					
40	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	1440
	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	
	465					470				475						480	
45	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	1488
	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
					485				490					495			
50	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	1536
	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	
				500				505						510			
55	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	1584
	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	
			515					520					525				
60	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	1633
	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	
		530					535					540					
	AA																1635

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

207

208

- (A) LENGTH: 544 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

10

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Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1           5           10           15
Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
          20          25          30
15 Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
    35          40          45
Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
    50          55          60
Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Lys Leu Tyr Leu Val Phe
20 65          70          75          80
Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
    85          90          95
Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
          100          105          110
25 Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
    115          120          125
Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
    130          135          140
Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
30 145          150          155          160
His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
    165          170          175
Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile Trp Ser Leu Gly Cys Ile
    180          185          190
35 Phe Ala Glu Met Val Thr Arg Arg Ala Leu Phe Pro Gly Asp Ser Glu
    195          200          205
Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr Leu Gly Thr Pro Asp Glu
    210          215          220
Val Val Trp Pro Gly Val Thr Ser Met Pro Asp Tyr Lys Pro Ser Phe
40 225          230          235          240
Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys Val Val Pro Pro Leu Asp
    245          250          255
Glu Asp Gly Arg Ser Leu Leu Ser Gln Met Leu His Tyr Asp Pro Asn
    260          265          270
45 Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala His Pro Phe Phe Gln Asp
    275          280          285
Val Thr Lys Pro Val Pro His Leu Arg Leu Trp Asp Pro Pro Val Ala
    290          295          300
Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
50 305          310          315          320
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
    325          330          335
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
    340          345          350
55 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
    355          360          365

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208

209

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 370 375 380
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 385 390 395 400
 5 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 405 410 415
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 420 425 430
 10 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 435 440 445
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 450 455 460
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 465 470 475 480
 15 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 485 490 495
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 500 505 510
 20 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 515 520 525
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 530 535 540

(2) INFORMATION FOR SEQ ID NO:114:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1635 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

35

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1632

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

40

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

45

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

50

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

55

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

209

210

	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
5	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
10	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
15	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
20	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
25	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
30	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
35	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
40	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
45	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
50	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
55	GGA CTC AGA TCT CGA GCC ATG GAG AAC TTC CAA AAG GTG GAA AAG ATC	768
	Gly Leu Arg Ser Arg Ala Met Glu Asn Phe Gln Lys Val Glu Lys Ile	
	245 250 255	
60	GGA GAG GGC ACG TAC GGA GTT GTG TAC AAA GCC AGA AAC AAG TTG ACG	816
	Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala Arg Asn Lys Leu Thr	
	260 265 270	
65	GGA GAG GTG GTG GCG CTT AAG AAA ATC CGC CTG GAC ACT GAG ACT GAG	864
	Gly Glu Val Val Ala Leu Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu	
	275 280 285	

211

	GGT GTG CCC AGT ACT GCC ATC CGA GAG ATC TCT CTG CTT AAG GAG CTT	912
	Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu	
	290 295 300	
5	AAC CAT CCT AAT ATT GTC AAG CTG CTG GAT GTC ATT CAC ACA GAA AAT	960
	Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn	
	305 310 315 320	
10	AAA CTC TAC CTG GTT TTT GAA TTT CTG CAC CAA GAT CTC AAG AAA TTC	1008
	Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe	
	325 330 335	
15	ATG GAT GCC TCT GCT CTC ACT GGC ATT CCT CTT CCC CTC ATC AAG AGC	1056
	Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser	
	340 345 350	
20	TAT CTG TTC CAG CTG CTC CAG GGC CTA GCT TTC TGC CAT TCT CAT CGG	1104
	Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg	
	355 360 365	
25	GTC CTC CAC CGA GAC CTT AAA CCT CAG AAT CTG CTT ATT AAC ACA GAG	1152
	Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu	
	370 375 380	
30	GGG GCC ATC AAG CTA GCA GAC TTT GGA CTA GCC AGA GCT TTT GGA GTC	1200
	Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val	
	385 390 395 400	
35	CCT GTT CGT ACT TAC ACC CAT GAG GTG GTG ACC CTG TGG TAC CGA GCT	1248
	Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala	
	405 410 415	
40	CCT GAA ATC CTC CTG GGC TCG AAA TAT TAT TCC ACA GCT GTG GAC ATC	1296
	Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile	
	420 425 430	
45	TGG AGC CTG GGC TGC ATC TTT GCT GAG ATG GTG ACT CGC CGG GCC CTG	1344
	Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu	
	435 440 445	
50	TTC CCT GGA GAT TCT GAG ATT GAC CAG CTC TTC CGG ATC TTT CGG ACT	1392
	Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr	
	450 455 460	
55	CTG GGG ACC CCA GAT GAG GTG GTG TGG CCA GGA GTT ACT TCT ATG CCT	1440
	Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro	
	465 470 475 480	
60	GAT TAC AAG CCA AGT TTC CCC AAG TGG GCC CGG CAA GAT TTT AGT AAA	1488
	Asp Tyr Lys Pro Ser Phe Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys	
	485 490 495	
65	GTT GTA CCT CCC CTG GAT GAA GAT GGA CGG AGC TTG TTA TCG CAA ATG	1536
	Val Val Pro Pro Leu Asp Glu Asp Gly Arg Ser Leu Leu Ser Gln Met	
	500 505 510	

211

212

CTG CAC TAC GAC CCT AAC AAG CGG ATT TCG GCC AAG GCA GCC CTG GCT 1584
 Leu His Tyr Asp Pro Asn Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala
 515 520 525

5 CAC CCT TTC TTC CAG GAT GTG ACC AAG CCA GTA CCC CAT CTT CGA CTC T 1633
 His Pro Phe Phe Gln Asp Val Thr Lys Pro Val Pro His Leu Arg Leu
 530 535 540

GA 1635

10

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 544 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

25 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 30 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 35 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 40 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 45 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 50 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Ala Met Glu Asn Phe Gln Lys Val Glu Lys Ile
 245 250 255
 55 Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala Arg Asn Lys Leu Thr

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		260		265		270											
		Gly	Glu	Val	Val	Ala	Leu	Lys	Lys	Ile	Arg	Leu	Asp	Thr	Glu	Thr	Glu
			275						280					285			
5		Gly	Val	Pro	Ser	Thr	Ala	Ile	Arg	Glu	Ile	Ser	Leu	Leu	Lys	Glu	Leu
			290					295					300				
		Asn	His	Pro	Asn	Ile	Val	Lys	Leu	Leu	Asp	Val	Ile	His	Thr	Glu	Asn
		305					310					315				320	
		Lys	Leu	Tyr	Leu	Val	Phe	Glu	Phe	Leu	His	Gln	Asp	Leu	Lys	Lys	Phe
					325					330					335		
10		Met	Asp	Ala	Ser	Ala	Leu	Thr	Gly	Ile	Pro	Leu	Pro	Leu	Ile	Lys	Ser
				340					345					350			
		Tyr	Leu	Phe	Gln	Leu	Leu	Gln	Gly	Leu	Ala	Phe	Cys	His	Ser	His	Arg
			355					360					365				
		Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Thr	Glu
15			370				375					380					
		Gly	Ala	Ile	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val
		385				390					395					400	
		Pro	Val	Arg	Thr	Tyr	Thr	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala
				405					410						415		
20		Pro	Glu	Ile	Leu	Leu	Gly	Ser	Lys	Tyr	Tyr	Ser	Thr	Ala	Val	Asp	Ile
				420					425					430			
		Trp	Ser	Leu	Gly	Cys	Ile	Phe	Ala	Glu	Met	Val	Thr	Arg	Arg	Ala	Leu
			435				440						445				
		Phe	Pro	Gly	Asp	Ser	Glu	Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Thr
25			450			455						460					
		Leu	Gly	Thr	Pro	Asp	Glu	Val	Val	Trp	Pro	Gly	Val	Thr	Ser	Met	Pro
		465				470					475					480	
		Asp	Tyr	Lys	Pro	Ser	Phe	Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys
				485					490					495			
30		Val	Val	Pro	Pro	Leu	Asp	Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met
				500					505					510			
		Leu	His	Tyr	Asp	Pro	Asn	Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala
			515					520					525				
		His	Pro	Phe	Phe	Gln	Asp	Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu
35			530				535					540					

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2532 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2529
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

55	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	48
	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10				15			

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	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
5	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
10	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
			50				55						60				
15	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75						80	
20	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTG	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
25	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
30	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
35	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					
40	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
45	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
50	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185						190			
55	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195				200					205				
60	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
			210				215					220					
65	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	

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215

	GGA CTC AGA TCT CGA GAG ATG CTG TCC CGT GGG TGG TTT CAC CGA GAC	768
	Gly Leu Arg Ser Arg Glu Met Leu Ser Arg Gly Trp Phe His Arg Asp	
	245 250 255	
5	CTC AGT GGG CTG GAT GCA GAG ACC CTG CTC AAG GGC CGA GGT GTC CAC	816
	Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys Gly Arg Gly Val His	
	260 265 270	
10	GGT AGC TTC CTG GCT CGG CCC AGT CGC AAG AAC CAG GGT GAC TTC TCG	864
	Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser	
	275 280 285	
15	CTC TCC GTC AGG GTG GGG GAT CAG GTG ACC CAT ATT CGG ATC CAG AAC	912
	Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile Gln Asn	
	290 295 300	
20	TCA GGG GAT TTC TAT GAC CTG TAT GGA GGG GAG AAG TTT GCG ACT CTG	960
	Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu	
	305 310 315 320	
25	ACA GAG CTG GTG GAG TAC TAC ACT CAG CAG CAG GGT GTC CTG CAG GAC	1008
	Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp	
	325 330 335	
30	CGC GAC GGC ACC ATC ATC CAC CTC AAG TAC CCG CTG AAC TGC TCC GAT	1056
	Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys Ser Asp	
	340 345 350	
35	CCC ACT AGT GAG AGG TGG TAC CAT GGC CAC ATG TCT GGC GGG CAG GCA	1104
	Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly Gln Ala	
	355 360 365	
40	GAG ACG CTG CTG CAG GCC AAG GGC GAG CCC TGG ACG TTT CTT GTG CGT	1152
	Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg	
	370 375 380	
45	GAG AGC CTC AGC CAG CCT GGA GAC TTC GTG CTT TCT GTG CTC AGT GAC	1200
	Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp	
	385 390 395 400	
50	CAG CCC AAG GCT GGC CCA GGC TCC CCG CTC AGG GTC ACC CAC ATC AAG	1248
	Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys	
	405 410 415	
55	GTC ATG TGC GAG GGT GGA CGC TAC ACA GTG GGT GGT TTG GAG ACC TTC	1296
	Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe	
	420 425 430	
60	GAC AGC CTC ACG GAC CTG GTA GAG CAT TTC AAG AAG ACG GGG ATT GAG	1344
	Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu	
	435 440 445	
65	GAG GCC TCA GGC GCC TTT GTC TAC CTG CGG CAG CCG TAC TAT GCC ACG	1392
	Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr	
	450 455 460	

215

216

5	AGG GTG AAT GCG GCT GAC ATT GAG AAC CGA GTG TTG GAA CTG AAC AAG	1440
	Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val Leu Glu Leu Asn Lys	
	465 470 475 480	
	AAG CAG GAG TCC GAG GAT ACA GCC AAG GCT GGC TTC TGG GAG GAG TTT	1488
	Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe	
10		
	GAG AGT TTG CAG AAG CAG GAG GTG AAG AAC TTG CAC CAG CGT CTG GAA	1536
	Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu His Gln Arg Leu Glu	
	500 505 510	
	GGG CAG CGG CCA GAG AAC AAG GGC AAG AAC CGC TAC AAG AAC ATT CTC	1584
15	Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu	
	515 520 525	
	CCC TTT GAC CAC AGC CGA GTG ATC CTG CAG GGA CGG GAC AGT AAC ATC	1632
	Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly Arg Asp Ser Asn Ile	
	530 535 540	
20	CCC GGG TCC GAC TAC ATC AAT GCC AAC TAC ATC AAG AAC CAG CTG CTA	1680
	Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu	
	545 550 555 560	
	GGC CCT GAT GAG AAC GCT AAG ACC TAC ATC GCC AGC CAG GGC TGT CTG	1728
	Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu	
25		
	GAG GCC ACG GTC AAT GAC TTC TGG CAG ATG GCG TGG CAG GAG AAC AGC	1776
	Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu Asn Ser	
	580 585 590	
	CGT GTC ATC GTC ATG ACC ACC CGA GAG GTG GAG AAA GGC CGG AAC AAA	1824
30	Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg Asn Lys	
	595 600 605	
	TGC GTC CCA TAC TGG CCC GAG GTG GGC ATG CAG CGT GCT TAT GGG CCC	1872
	Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln Arg Ala Tyr Gly Pro	
	610 615 620	
35	TAC TCT GTG ACC AAC TGC GGG GAG CAT GAC ACA ACC GAA TAC AAA CTC	1920
	Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr Lys Leu	
	625 630 635 640	
	CGT ACC TTA CAG GTC TCC CCG CTG GAC AAT GGA GAC CTG ATT CGG GAG	1968
	Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu	
40		
	ATC TGG CAT TAC CAG TAC CTG AGC TGG CCC GAC CAT GGG GTC CCC AGT	2016
	Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His Gly Val Pro Ser	
	660 665 670	
	GAG CCT GGG GGT GTC CTC AGC TTC CTG GAC CAG ATC AAC CAG CGG CAG	2064
45	Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln	
	675 680 685	

216

217

5 GAA AGT CTG CCT CAC GCA GGG CCC ATC ATC GTG CAC TGC AGC GCC GGC 2112
 Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser Ala Gly
 690 695 700

10 ATC GGC CGC ACA GGC ACC ATC ATT GTC ATC GAC ATG CTC ATG GAG AAC 2160
 Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met Glu Asn
 705 710 715 720

15 ATC TCC ACC AAG GGC CTG GAC TGT GAC ATT GAC ATC CAG AAG ACC ATC 2208
 Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile
 725 730 735

20 CAG ATG GTG CGG GCG CAG CGC TCG GGC ATG GTG CAG ACG GAG GCG CAG 2256
 Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln
 740 745 750

25 TAC AAG TTC ATC TAC GTG GCC ATC GCC CAG TTC ATT GAA ACC ACT AAG 2304
 Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys
 755 760 765

30 AAG AAG CTG GAG GTC CTG CAG TCG CAG AAG GGC CAG GAG TCG GAG TAC 2352
 Lys Lys Leu Glu Val Leu Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr
 770 775 780

35 GGG AAC ATC ACC TAT CCC CCA GCC ATG AAG AAT GCC CAT GCC AAG GCC 2400
 Gly Asn Ile Thr Tyr Pro Pro Ala Met Lys Asn Ala His Ala Lys Ala
 785 790 795 800

40 TCC CGC ACC TCG TCC AAA CAC AAG GAG GAT GTG TAT GAG AAC CTG CAC 2448
 Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val Tyr Glu Asn Leu His
 805 810 815

45 ACT AAG AAC AAG AGG GAG GAG AAA GTG AAG AAG CAG CGG TCA GCA GAC 2496
 Thr Lys Asn Lys Arg Glu Glu Lys Val Lys Lys Gln Arg Ser Ala Asp
 820 825 830

50 AAG GAG AAG AGC AAG GGT TCC CTC AAG AGG AAG TGA 2532
 Lys Glu Lys Ser Lys Gly Ser Leu Lys Arg Lys
 835 840

(2) INFORMATION FOR SEQ ID NO:117:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 50 (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

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	1				5				10					15			
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
5	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75						80	
10	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
15	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150						155					160	
20	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165						170					175		
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180						185					190			
25	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
		195					200						205				
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225				230						235					240	
30	Gly	Leu	Arg	Ser	Arg	Glu	Met	Leu	Ser	Arg	Gly	Trp	Phe	His	Arg	Asp	
					245					250					255		
	Leu	Ser	Gly	Leu	Asp	Ala	Glu	Thr	Leu	Leu	Lys	Gly	Arg	Gly	Val	His	
			260						265					270			
35	Gly	Ser	Phe	Leu	Ala	Arg	Pro	Ser	Arg	Lys	Asn	Gln	Gly	Asp	Phe	Ser	
		275					280					285					
	Leu	Ser	Val	Arg	Val	Gly	Asp	Gln	Val	Thr	His	Ile	Arg	Ile	Gln	Asn	
		290					295					300					
	Ser	Gly	Asp	Phe	Tyr	Asp	Leu	Tyr	Gly	Gly	Glu	Lys	Phe	Ala	Thr	Leu	
	305				310						315					320	
40	Thr	Glu	Leu	Val	Glu	Tyr	Tyr	Thr	Gln	Gln	Gln	Gly	Val	Leu	Gln		

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	450		455		460														
	Arg	Val	Asn	Ala	Ala	Asp	Ile	Glu	Asn	Arg	Val	Leu	Glu	Leu	Asn	Lys			
	465					470					475				480				
5	Lys	Gln	Glu	Ser	Glu	Asp	Thr	Ala	Lys	Ala	Gly	Phe	Trp	Glu	Glu	Phe			
					485					490					495				
	Glu	Ser	Leu	Gln	Lys	Gln	Glu	Val	Lys	Asn	Leu	His	Gln	Arg	Leu	Glu			
				500					505					510					
	Gly	Gln	Arg	Pro	Glu	Asn	Lys	Gly	Lys	Asn	Arg	Tyr	Lys	Asn	Ile	Leu			
			515					520					525						
10	Pro	Phe	Asp	His	Ser	Arg	Val	Ile	Leu	Gln	Gly	Arg	Asp	Ser	Asn	Ile			
		530					535					540							
	Pro	Gly	Ser	Asp	Tyr	Ile	Asn	Ala	Asn	Tyr	Ile	Lys	Asn	Gln	Leu	Leu			
	545					550					555				560				
15	Gly	Pro	Asp	Glu	Asn	Ala	Lys	Thr	Tyr	Ile	Ala	Ser	Gln	Gly	Cys	Leu			
					565					570					575				
	Glu	Ala	Thr	Val	Asn	Asp	Phe	Trp	Gln	Met	Ala	Trp	Gln	Glu	Asn	Ser			
				580					585					590					
	Arg	Val	Ile	Val	Met	Thr	Thr	Arg	Glu	Val	Glu	Lys	Gly	Arg	Asn	Lys			
			595					600					605						
20	Cys	Val	Pro	Tyr	Trp	Pro	Glu	Val	Gly	Met	Gln	Arg	Ala	Tyr	Gly	Pro			
		610					615				620								
	Tyr	Ser	Val	Thr	Asn	Cys	Gly	Glu	His	Asp	Thr	Thr	Glu	Tyr	Lys	Leu			
	625				630					635					640				
	Arg	Thr	Leu	Gln	Val	Ser	Pro	Leu	Asp	Asn	Gly	Asp	Leu	Ile	Arg	Glu			
25					645					650					655				
	Ile	Trp	His	Tyr	Gln	Tyr	Leu	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Ser			
				660					665				670						
	Glu	Pro	Gly	Gly	Val	Leu	Ser	Phe	Leu	Asp	Gln	Ile	Asn	Gln	Arg	Gln			
			675					680				685							
30	Glu	Ser	Leu	Pro	His	Ala	Gly	Pro	Ile	Ile	Val	His	Cys	Ser	Ala	Gly			
		690					695				700								
	Ile	Gly	Arg	Thr	Gly	Thr	Ile	Ile	Val	Ile	Asp	Met	Leu	Met	Glu	Asn			
	705				710					715					720				
	Ile	Ser	Thr	Lys	Gly	Leu	Asp	Cys	Asp	Ile	Asp	Ile	Gln	Lys	Thr	Ile			
35					725					730					735				
	Gln	Met	Val	Arg	Ala	Gln	Arg	Ser	Gly	Met	Val	Gln	Thr	Glu	Ala	Gln			
				740					745				750						
	Tyr	Lys	Phe	Ile	Tyr	Val	Ala	Ile	Ala	Gln	Phe	Ile	Glu	Thr	Thr	Lys			
		755					760				765								
40	Lys	Lys	Leu	Glu	Val	Leu	Gln	Ser	Gln	Lys	Gly	Gln	Glu	Ser	Glu	Tyr			
		770					775				780								
	Gly	Asn	Ile	Thr	Tyr	Pro	Ala	Met	Lys	Asn	Ala	His	Ala	Lys	Ala				
	785				790					795					800				
	Ser	Arg	Thr	Ser	Ser	Lys	His	Lys	Glu	Asp	Val	Tyr	Glu	Asn	Leu	His			
45					805					810					815				
	Thr	Lys	Asn	Lys	Arg	Glu	Glu	Lys	Val	Lys	Lys	Gln	Arg	Ser	Ala	Asp			
				820					825					830					
	Lys	Glu	Lys	Ser	Lys	Gly	Ser	Leu	Lys	Arg	Lys								
		835					840												

50

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2562 base pairs

55

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

219

220

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2559

(D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATG CTG TCC CGT GGG TGG TTT CAC CGA GAC CTC AGT GGG CTG GAT GCA	48
Met Leu Ser Arg Gly Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala	
1 5 10 15	

15

GAG ACC CTG CTC AAG GGC CGA GGT GTC CAC GGT AGC TTC CTG GCT CGG	96
Glu Thr Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg	
20 25 30	

20

CCC AGT CGC AAG AAC CAG GGT GAC TTC TCG CTC TCC GTC AGG GTG GGG	144
Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly	
35 40 45	

25

GAT CAG GTG ACC CAT ATT CGG ATC CAG AAC TCA GGG GAT TTC TAT GAC	192
Asp Gln Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp	
50 55 60	

30

CTG TAT GGA GGG GAG AAG TTT GCG ACT CTG ACA GAG CTG GTG GAG TAC	240
Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr	
65 70 75 80	

35

TAC ACT CAG CAG CAG GGT GTC CTG CAG GAC CGC GAC GGC ACC ATC ATC	288
Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile	
85 90 95	

40

CAC CTC AAG TAC CCG CTG AAC TGC TCC GAT CCC ACT AGT GAG AGG TGG	336
His Leu Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp	
100 105 110	

45

TAC CAT GGC CAC ATG TCT GGC GGG CAG GCA GAG ACG CTG CTG CAG GCC	384
Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala	
115 120 125	

50

AAG GGC GAG CCC TGG ACG TTT CTT GTG CGT GAG AGC CTC AGC CAG CCT	432
Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro	
130 135 140	

55

GGA GAC TTC GTG CTT TCT GTG CTC AGT GAC CAG CCC AAG GCT GGC CCA	480
Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro	
145 150 155 160	

GGC TCC CCG CTC AGG GTC ACC CAC ATC AAG GTC ATG TGC GAG GGT GGA	528
Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly	
165 170 175	

55

CGC TAC ACA GTG GGT GGT TTG GAG ACC TTC GAC AGC CTC ACG GAC CTG	576
-----------------------------------------------------------------	-----

220

221

	Arg	Tyr	Thr	Val	Gly	Gly	Leu	Glu	Thr	Phe	Asp	Ser	Leu	Thr	Asp	Leu	
				180					185					190			
5	GTA	GAG	CAT	TTC	AAG	AAG	ACG	GGG	ATT	GAG	GAG	GCC	TCA	GGC	GCC	TTT	624
	Val	Glu	His	Phe	Lys	Lys	Thr	Gly	Ile	Glu	Glu	Ala	Ser	Gly	Ala	Phe	
				195				200					205				
10	GTC	TAC	CTG	CGG	CAG	CCG	TAC	TAT	GCC	ACG	AGG	GTG	AAT	GCG	GCT	GAC	672
	Val	Tyr	Leu	Arg	Gln	Pro	Tyr	Tyr	Ala	Thr	Arg	Val	Asn	Ala	Ala	Asp	
				210				215					220				
15	ATT	GAG	AAC	CGA	GTG	TTG	GAA	CTG	AAC	AAG	AAG	CAG	GAG	TCC	GAG	GAT	720
	Ile	Glu	Asn	Arg	Val	Leu	Glu	Leu	Asn	Lys	Lys	Gln	Glu	Ser	Glu	Asp	
						230					235				240		
	ACA	GCC	AAG	GCT	GGC	TTC	TGG	GAG	GAG	TTT	GAG	AGT	TTG	CAG	AAG	CAG	768
	Thr	Ala	Lys	Ala	Gly	Phe	Trp	Glu	Glu	Phe	Glu	Ser	Leu	Gln	Lys	Gln	
					245					250					255		
20	GAG	GTG	AAG	AAC	TTG	CAC	CAG	CGT	CTG	GAA	GGG	CAG	CGG	CCA	GAG	AAC	816
	Glu	Val	Lys	Asn	Leu	His	Gln	Arg	Leu	Glu	Gly	Gln	Arg	Pro	Glu	Asn	
				260					265					270			
25	AAG	GGC	AAG	AAC	CGC	TAC	AAG	AAC	ATT	CTC	CCC	TTT	GAC	CAC	AGC	CGA	864
	Lys	Gly	Lys	Asn	Arg	Tyr	Lys	Asn	Ile	Leu	Pro	Phe	Asp	His	Ser	Arg	
				275				280					285				
30	GTG	ATC	CTG	CAG	GGA	CGG	GAC	AGT	AAC	ATC	CCC	GGG	TCC	GAC	TAC	ATC	912
	Val	Ile	Leu	Gln	Gly	Arg	Asp	Ser	Asn	Ile	Pro	Gly	Ser	Asp	Tyr	Ile	
				290				295				300					
35	AAT	GCC	AAC	TAC	ATC	AAG	AAC	CAG	CTG	CTA	GGC	CCT	GAT	GAG	AAC	GCT	960
	Asn	Ala	Asn	Tyr	Ile	Lys	Asn	Gln	Leu	Leu	Gly	Pro	Asp	Glu	Asn	Ala	
				305			310				315				320		
	AAG	ACC	TAC	ATC	GCC	AGC	CAG	GGC	TGT	CTG	GAG	GCC	ACG	GTC	AAT	GAC	1008
	Lys	Thr	Tyr	Ile	Ala	Ser	Gln	Gly	Cys	Leu	Glu	Ala	Thr	Val	Asn	Asp	
					325				330						335		
40	TTC	TGG	CAG	ATG	GCG	TGG	CAG	GAG	AAC	AGC	CGT	GTC	ATC	GTC	ATG	ACC	1056
	Phe	Trp	Gln	Met	Ala	Trp	Gln	Glu	Asn	Ser	Arg	Val	Ile	Val	Met	Thr	
				340					345					350			
45	ACC	CGA	GAG	GTG	GAG	AAA	GGC	CGG	AAC	AAA	TGC	GTC	CCA	TAC	TGG	CCC	1104
	Thr	Arg	Glu	Val	Glu	Lys	Gly	Arg	Asn	Lys	Cys	Val	Pro	Tyr	Trp	Pro	
				355				360					365				
50	GAG	GTG	GGC	ATG	CAG	CGT	GCT	TAT	GGG	CCC	TAC	TCT	GTG	ACC	AAC	TGC	1152
	Glu	Val	Gly	Met	Gln	Arg	Ala	Tyr	Gly	Pro	Tyr	Ser	Val	Thr	Asn	Cys	
				370			375					380					
55	GGG	GAG	CAT	GAC	ACA	ACC	GAA	TAC	AAA	CTC	CGT	ACC	TTA	CAG	GTC	TCC	1200
	Gly	Glu	His	Asp	Thr	Thr	Glu	Tyr	Lys	Leu	Arg	Thr	Leu	Gln	Val	Ser	
						390					395				400		
	CCG	CTG	GAC	AAT	GGA	GAC	CTG	ATT	CGG	GAG	ATC	TGG	CAT	TAC	CAG	TAC	1248

221

222

	Pro	Leu	Asp	Asn	Gly	Asp	Leu	Ile	Arg	Glu	Ile	Trp	His	Tyr	Gln	Tyr	
					405					410					415		
5	CTG	AGC	TGG	CCC	GAC	CAT	GGG	GTC	CCC	AGT	GAG	CCT	GGG	GGT	GTC	CTC	1296
	Leu	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Ser	Glu	Pro	Gly	Gly	Val	Leu	
				420				425					430				
10	AGC	TTC	CTG	GAC	CAG	ATC	AAC	CAG	CGG	CAG	GAA	AGT	CTG	CCT	CAC	GCA	1344
	Ser	Phe	Leu	Asp	Gln	Ile	Asn	Gln	Arg	Gln	Glu	Ser	Leu	Pro	His	Ala	
			435					440					445				
15	GGG	CCC	ATC	ATC	GTG	CAC	TGC	AGC	GCC	GGC	ATC	GGC	CGC	ACA	GGC	ACC	1392
	Gly	Pro	Ile	Ile	Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Thr	
		450					455					460					
20	ATC	ATT	GTC	ATC	GAC	ATG	CTC	ATG	GAG	AAC	ATC	TCC	ACC	AAG	GGC	CTG	1440
	Ile	Ile	Val	Ile	Asp	Met	Leu	Met	Glu	Asn	Ile	Ser	Thr	Lys	Gly	Leu	
	465					470					475					480	
25	GAC	TGT	GAC	ATT	GAC	ATC	CAG	AAG	ACC	ATC	CAG	ATG	GTG	CGG	GCG	CAG	1488
	Asp	Cys	Asp	Ile	Asp	Ile	Gln	Lys	Thr	Ile	Gln	Met	Val	Arg	Ala	Gln	
					485					490					495		
30	CGC	TCG	GGC	ATG	GTG	CAG	ACG	GAG	GCG	CAG	TAC	AAG	TTC	ATC	TAC	GTG	1536
	Arg	Ser	Gly	Met	Val	Gln	Thr	Glu	Ala	Gln	Tyr	Lys	Phe	Ile	Tyr	Val	
				500					505					510			
35	GCC	ATC	GCC	CAG	TTC	ATT	GAA	ACC	ACT	AAG	AAG	AAG	CTG	GAG	GTC	CTG	1584
	Ala	Ile	Ala	Gln	Phe	Ile	Glu	Thr	Thr	Lys	Lys	Lys	Leu	Glu	Val	Leu	
			515					520					525				
40	CAG	TCG	CAG	AAG	GGC	CAG	GAG	TCG	GAG	TAC	GGG	AAC	ATC	ACC	TAT	CCC	1632
	Gln	Ser	Gln	Lys	Gly	Gln	Glu	Ser	Glu	Tyr	Gly	Asn	Ile	Thr	Tyr	Pro	
			530				535					540					
45	CCA	GCC	ATG	AAG	AAT	GCC	CAT	GCC	AAG	GCC	TCC	CGC	ACC	TCG	TCC	AAA	1680
	Pro	Ala	Met	Lys	Asn	Ala	His	Ala	Lys	Ala	Ser	Arg	Thr	Ser	Ser	Lys	
	545					550					555					560	
50	CAC	AAG	GAG	GAT	GTG	TAT	GAG	AAC	CTG	CAC	ACT	AAG	AAC	AAG	AGG	GAG	1728
	His	Lys	Glu	Asp	Val	Tyr	Glu	Asn	Leu	His	Thr	Lys	Asn	Lys	Arg	Glu	
					565				570					575			
55	GAG	AAA	GTG	AAG	AAG	CAG	CGG	TCA	GCA	GAC	AAG	GAG	AAG	AGC	AAG	GGT	1776
	Glu	Lys	Val	Lys	Lys	Gln	Arg	Ser	Ala	Asp	Lys	Glu	Lys	Ser	Lys	Gly	
				580					585					590			
60	TCC	CTC	AAG	AGG	AAG	CGA	ATT	CTG	CAG	TCG	ACG	GTA	CCG	CGG	GCC	CGG	1824
	Ser	Leu	Lys	Arg	Lys	Arg	Ile	Leu	Gln	Ser	Thr	Val	Pro	Arg	Ala	Arg	
			595					600					605				
65	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	1872
	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	
		610					615					620					
70	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	1920

222

223

	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	
	625					630					635					640	
5	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	1968
	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	
					645					650					655		
10	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	2016
	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	
				660						665				670			
15	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	2064
	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	
			675					680					685				
	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	2112
	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	
		690					695					700					
20	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	2160
	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	
	705					710					715					720	
25	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	2208
	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	
				725						730					735		
30	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	2256
	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	
			740					745						750			
35	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	2304
	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	
			755					760					765				
	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	2352
	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	
		770					775					780					
40	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	2400
	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	
	785					790					795					800	
45	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	2448
	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	
				805						810					815		
50	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	2496
	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	
			820						825					830			
55	ATG	GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	2544
	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	
			835					840					845				
	GAC	GAG	CTG	TAC	AAG	TAA											2562
																	223

224

Asp Glu Leu Tyr Lys
850

5 (2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 853 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

	Met	Leu	Ser	Arg	Gly	Trp	Phe	His	Arg	Asp	Leu	Ser	Gly	Leu	Asp	Ala	
	1				5					10					15		
20	Glu	Thr	Leu	Leu	Lys	Gly	Arg	Gly	Val	His	Gly	Ser	Phe	Leu	Ala	Arg	
				20					25					30			
	Pro	Ser	Arg	Lys	Asn	Gln	Gly	Asp	Phe	Ser	Leu	Ser	Val	Arg	Val	Gly	
				35				40					45				
25	Asp	Gln	Val	Thr	His	Ile	Arg	Ile	Gln	Asn	Ser	Gly	Asp	Phe	Tyr	Asp	
		50					55					60					
	Leu	Tyr	Gly	Gly	Glu	Lys	Phe	Ala	Thr	Leu	Thr	Glu	Leu	Val	Glu	Tyr	
	65					70					75				80		
	Tyr	Thr	Gln	Gln	Gln	Gly	Val	Leu	Gln	Asp	Arg	Asp	Gly	Thr	Ile	Ile	
					85					90					95		
30	His	Leu	Lys	Tyr	Pro	Leu	Asn	Cys	Ser	Asp	Pro	Thr	Ser	Glu	Arg	Trp	
				100						105				110			
	Tyr	His	Gly	His	Met	Ser	Gly	Gly	Gln	Ala	Glu	Thr	Leu	Leu	Gln	Ala	
			115				120						125				
35	Lys	Gly	Glu	Pro	Trp	Thr	Phe	Leu	Val	Arg	Glu	Ser	Leu	Ser	Gln	Pro	
		130					135						140				
	Gly	Asp	Phe	Val	Leu	Ser	Val	Leu	Ser	Asp	Gln	Pro	Lys	Ala	Gly	Pro	
	145					150					155				160		
	Gly	Ser	Pro	Leu	Arg	Val	Thr	His	Ile	Lys	Val	Met	Cys	Glu	Gly	Gly	
					165					170					175		
40	Arg	Tyr	Thr	Val	Gly	Gly	Leu	Glu	Thr	Phe	Asp	Ser	Leu	Thr	Asp	Leu	
				180						185					190		
	Val	Glu	His	Phe	Lys	Lys	Thr	Gly	Ile	Glu	Glu	Ala	Ser	Gly	Ala	Phe	
			195					200					205				
45	Val	Tyr	Leu	Arg	Gln	Pro	Tyr	Tyr	Ala	Thr	Arg	Val	Asn	Ala	Ala	Asp	
		210					215						220				
	Ile	Glu	Asn	Arg	Val	Leu	Glu	Leu	Asn	Lys	Lys	Gln	Glu	Ser	Glu	Asp	
	225					230						235			240		
	Thr	Ala	Lys	Ala	Gly	Phe	Trp	Glu	Glu	Phe	Glu	Ser	Leu	Gln	Lys	Gln	
					245					250					255		
50	Glu	Val	Lys	Asn	Leu	His	Gln	Arg	Leu	Glu	Gly	Gln	Arg	Pro	Glu	Asn	
				260					265					270			
	Lys	Gly	Lys	Asn	Arg	Tyr	Lys	Asn	Ile	Leu	Pro	Phe	Asp	His	Ser	Arg	
			275					280					285				
	Val	Ile	Leu	Gln	Gly	Arg	Asp	Ser	Asn	Ile	Pro	Gly	Ser	Asp	Tyr	Ile	
55		290					295					300					
	Asn	Ala	Asn	Tyr	Ile	Lys	Asn	Gln	Leu	Leu	Gly	Pro	Asp	Glu	Asn	Ala	

224

225

	305		310		315		320
	Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp						
		325		330		335	
5	Phe Trp Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr						
		340		345		350	
	Thr Arg Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro						
		355		360		365	
	Glu Val Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys						
		370		375		380	
10	Gly Glu His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser						
		385		390		395	
	Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr						
		405		410		415	
	Leu Ser Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu						
15		420		425		430	
	Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala						
		435		440		445	
	Gly Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr						
		450		455		460	
20	Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu						
		465		470		475	
	Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln						
		485		490		495	
	Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val						
25		500		505		510	
	Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu						
		515		520		525	
	Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro						
		530		535		540	
30	Pro Ala Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys						
		545		550		555	
	His Lys Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu						
		565		570		575	
	Glu Lys Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly						
35		580		585		590	
	Ser Leu Lys Arg Lys Arg Ile Leu Gln Ser Thr Val Pro Arg Ala Arg						
		595		600		605	
	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr						
		610		615		620	
40	Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His						
		625		630		635	
	Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys						
		645		650		655	
	Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp						
45		660		665		670	
	Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg						
		675		680		685	
	Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro						
		690		695		700	
50	Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn						
		705		710		715	
	Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn						
		725		730		735	
	Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu						
55		740		745		750	
	Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met						

225

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755 760 765
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
 770 775 780
 5 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 785 790 795 800
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 805 810 815
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 820 825 830
 10 Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
 835 840 845
 Asp Glu Leu Tyr Lys
 850

15 (2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2994 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2991

(D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336

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	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
5	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
10	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					
15	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
20	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165					170					175		
25	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
30	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
35	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
			210				215					220					
40	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235					240		
45	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCG	AAT	TCG	ACC	ATG	GAG	CGG	CCC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Glu	Arg	Pro	
					245				250					255			
50	CCG	GGG	CTG	CGG	CCG	GGC	GCG	GGC	GGG	CCC	TGG	GAG	ATG	CGG	GAG	CGG	816
	Pro	Gly	Leu	Arg	Pro	Gly	Ala	Gly	Gly	Pro	Trp	Glu	Met	Arg	Glu	Arg	
				260				265						270			
55	CTG	GGC	ACC	GGC	GGC	TTC	GGG	AAC	GTC	TGT	CTG	TAC	CAG	CAT	CGG	GAA	864
	Leu	Gly	Thr	Gly	Gly	Phe	Gly	Asn	Val	Cys	Leu	Tyr	Gln	His	Arg	Glu	
			275				280						285				
60	CTT	GAT	CTC	AAA	ATA	GCA	ATT	AAG	TCT	TGT	CGC	CTA	GAG	CTA	AGT	ACC	912
	Leu	Asp	Leu	Lys	Ile	Ala	Ile	Lys	Ser	Cys	Arg	Leu	Glu	Leu	Ser	Thr	
			290				295					300					
65	AAA	AAC	AGA	GAA	CGA	TGG	TGC	CAT	GAA	ATC	CAG	ATT	ATG	AAG	AAG	TTG	960
	Lys	Asn	Arg	Glu	Arg	Trp	Cys	His	Glu	Ile	Gln	Ile	Met	Lys	Lys	Leu	
	305					310				315						320	
70	AAC	CAT	GCC	AAT	GTT	GTA	AAG	GCC	TGT	GAT	GTT	CCT	GAA	GAA	TTG	AAT	1008

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	Asn	His	Ala	Asn	Val	Val	Lys	Ala	Cys	Asp	Val	Pro	Glu	Glu	Leu	Asn	
					325					330					335		
5	ATT	TTG	ATT	CAT	GAT	GTG	CCT	CTT	CTA	GCA	ATG	GAA	TAC	TGT	TCT	GGA	1056
	Ile	Leu	Ile	His	Asp	Val	Pro	Leu	Leu	Ala	Met	Glu	Tyr	Cys	Ser	Gly	
				340				345					350				
10	GGA	GAT	CTC	CGA	AAG	CTG	CTC	AAC	AAA	CCA	GAA	AAT	TGT	TGT	GGA	CTT	1104
	Gly	Asp	Leu	Arg	Lys	Leu	Leu	Asn	Lys	Pro	Glu	Asn	Cys	Cys	Gly	Leu	
			355					360					365				
15	AAA	GAA	AGC	CAG	ATA	CTT	TCT	TTA	CTA	AGT	GAT	ATA	GGG	TCT	GGG	ATT	1152
	Lys	Glu	Ser	Gln	Ile	Leu	Ser	Leu	Leu	Ser	Asp	Ile	Gly	Ser	Gly	Ile	
		370					375				380						
20	CGA	TAT	TTG	CAT	GAA	AAC	AAA	ATT	ATA	CAT	CGA	GAT	CTA	AAA	CCT	GAA	1200
	Arg	Tyr	Leu	His	Glu	Asn	Lys	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Glu	
	385					390					395				400		
25	AAC	ATA	GTT	CTT	CAG	GAT	GTT	GGT	GGA	AAG	ATA	ATA	CAT	AAA	ATA	ATT	1248
	Asn	Ile	Val	Leu	Gln	Asp	Val	Gly	Gly	Lys	Ile	Ile	His	Lys	Ile	Ile	
				405				410							415		
30	GAT	CTG	GGA	TAT	GCC	AAA	GAT	GTT	GAT	CAA	GGA	AGT	CTG	TGT	ACA	TCT	1296
	Asp	Leu	Gly	Tyr	Ala	Lys	Asp	Val	Asp	Gln	Gly	Ser	Leu	Cys	Thr	Ser	
			420					425					430				
35	TTT	GTG	GGA	ACA	CTG	CAG	TAT	CTG	GCC	CCA	GAG	CTC	TTT	GAG	AAT	AAG	1344
	Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu	Phe	Glu	Asn	Lys	
		435					440					445					
40	CCT	TAC	ACA	GCC	ACT	GTT	GAT	TAT	TGG	AGC	TTT	GGG	ACC	ATG	GTA	TTT	1392
	Pro	Tyr	Thr	Ala	Thr	Val	Asp	Tyr	Trp	Ser	Phe	Gly	Thr	Met	Val	Phe	
		450					455					460					
45	GAA	TGT	ATT	GCT	GGA	TAT	AGG	CCT	TTT	TTG	CAT	CAT	CTG	CAG	CCA	TTT	1440
	Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His	Leu	Gln	Pro	Phe	
	465				470				475				480				
50	ACC	TGG	CAT	GAG	AAG	ATT	AAG	AAG	AAG	GAT	CCA	AAG	TGT	ATA	TTT	GCA	1488
	Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys	Cys	Ile	Phe	Ala	
				485				490					495				
55	TGT	GAA	GAG	ATG	TCA	GGA	GAA	GTT	CGG	TTT	AGT	AGC	CAT	TTA	CCT	CAA	1536
	Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser	His	Leu	Pro	Gln	
			500					505					510				
60	CCA	AAT	AGC	CTT	TGT	AGT	TTA	ATA	GTA	GAA	CCC	ATG	GAA	AAC	TGG	CTA	1584
	Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met	Glu	Asn	Trp	Leu	
		515					520						525				
65	CAG	TTG	ATG	TTG	AAT	TGG	GAC	CCT	CAG	CAG	AGA	GGA	GGA	CCT	GTT	GAC	1632
	Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly	Gly	Pro	Val	Asp	
		530					535					540					
70	CTT	ACT	TTG	AAG	CAG	CCA	AGA	TGT	TTT	GTA	TTA	ATG	GAT	CAC	ATT	TTG	1680

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	Leu	Thr	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met	Asp	His	Ile	Leu	
	545					550					555					560	
5	AAT	TTG	AAG	ATA	GTA	CAC	ATC	CTA	AAT	ATG	ACT	TCT	GCA	AAG	ATA	ATT	1728
	Asn	Leu	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser	Ala	Lys	Ile	Ile	
					565					570					575		
10	TCT	TTT	CTG	TTA	CCA	CCT	GAT	GAA	AGT	CTT	CAT	TCA	CTA	CAG	TCT	CGT	1776
	Ser	Phe	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser	Leu	Gln	Ser	Arg	
				580					585					590			
15	ATT	GAG	CGT	GAA	ACT	GGA	ATA	AAT	ACT	GGT	TCT	CAA	GAA	CTT	CTT	TCA	1824
	Ile	Glu	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln	Glu	Leu	Leu	Ser	
			595					600					605				
	GAG	ACA	GGA	ATT	TCT	CTG	GAT	CCT	CGG	AAA	CCA	GCC	TCT	CAA	TGT	GTT	1872
	Glu	Thr	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala	Ser	Gln	Cys	Val	
		610					615					620					
20	CTA	GAT	GGA	GTT	AGA	GGC	TGT	GAT	AGC	TAT	ATG	GTT	TAT	TTG	TTT	GAT	1920
	Leu	Asp	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Val	Tyr	Leu	Phe	Asp	
						630					635					640	
25	AAA	AGT	AAA	ACT	GTA	TAT	GAA	GGG	CCA	TTT	GCT	TCC	AGA	AGT	TTA	TCT	1968
	Lys	Ser	Lys	Thr	Val	Tyr	Glu	Gly	Pro	Phe	Ala	Ser	Arg	Ser	Leu	Ser	
					645					650					655		
30	GAT	TGT	GTA	AAT	TAT	ATT	GTA	CAG	GAC	AGC	AAA	ATA	CAG	CTT	CCA	ATT	2016
	Asp	Cys	Val	Asn	Tyr	Ile	Val	Gln	Asp	Ser	Lys	Ile	Gln	Leu	Pro	Ile	
				660					665					670			
35	ATA	CAG	CTG	CGT	AAA	GTG	TGG	GCT	GAA	GCA	GTG	CAC	TAT	GTG	TCT	GGA	2064
	Ile	Gln	Leu	Arg	Lys	Val	Trp	Ala	Glu	Ala	Val	His	Tyr	Val	Ser	Gly	
			675					680					685				
	CTA	AAA	GAA	GAC	TAT	AGC	AGG	CTC	TTT	CAG	GGA	CAA	AGG	GCA	GCA	ATG	2112
	Leu	Lys	Glu	Asp	Tyr	Ser	Arg	Leu	Phe	Gln	Gly	Gln	Arg	Ala	Ala	Met	
			690				695					700					
40	TTA	AGT	CTT	CTT	AGA	TAT	AAT	GCT	AAC	TTA	ACA	AAA	ATG	AAG	AAC	ACT	2160
	Leu	Ser	Leu	Leu	Arg	Tyr	Asn	Ala	Asn	Leu	Thr	Lys	Met	Lys	Asn	Thr	
		705				710					715					720	
45	TTG	ATC	TCA	GCA	TCA	CAA	CAA	CTG	AAA	GCT	AAA	TTG	GAG	TTT	TTT	CAC	2208
	Leu	Ile	Ser	Ala	Ser	Gln	Gln	Leu	Lys	Ala	Lys	Leu	Glu	Phe	Phe	His	
					725					730					735		
50	AAA	AGC	ATT	CAG	CTT	GAC	TTG	GAG	AGA	TAC	AGC	GAG	CAG	ATG	ACG	TAT	2256
	Lys	Ser	Ile	Gln	Leu	Asp	Leu	Glu	Arg	Tyr	Ser	Glu	Gln	Met	Thr	Tyr	
				740					745					750			
55	GGG	ATA	TCT	TCA	GAA	AAA	ATG	CTA	AAA	GCA	TGG	AAA	GAA	ATG	GAA	GAA	2304
	Gly	Ile	Ser	Ser	Glu	Lys	Met	Leu	Lys	Ala	Trp	Lys	Glu	Met	Glu	Glu	
			755					760					765				
	AAG	GCC	ATC	CAC	TAT	GCT	GAG	GTT	GGT	GTC	ATT	GGA	TAC	CTG	GAG	GAT	2352

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	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly	Tyr	Leu	Glu	Asp	
	770						775					780					
5	CAG	ATT	ATG	TCT	TTG	CAT	GCT	GAA	ATC	ATG	GGG	CTA	CAG	AAG	AGC	CCC	2400
	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Gly	Leu	Gln	Lys	Ser	Pro	
	785					790					795					800	
10	TAT	GGA	AGA	CGT	CAG	GGA	GAC	TTG	ATG	GAA	TCT	CTG	GAA	CAG	CGT	GCC	2448
	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu	Glu	Gln	Arg	Ala	
					805					810						815	
15	ATT	GAT	CTA	TAT	AAG	CAG	TTA	AAA	CAC	AGA	CCT	TCA	GAT	CAC	TCC	TAC	2496
	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser	Asp	His	Ser	Tyr	
					820				825						830		
20	AGT	GAC	AGC	ACA	GAG	ATG	GTG	AAA	ATC	ATT	GTG	CAC	ACT	GTG	CAG	AGT	2544
	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His	Thr	Val	Gln	Ser	
					835			840						845			
25	CAG	GAC	CGT	GTG	CTC	AAG	GAG	CTG	TTT	GGT	CAT	TTG	AGC	AAG	TTG	TTG	2592
	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu	Ser	Lys	Leu	Leu	
		850					855					860					
30	GGC	TGT	AAG	CAG	AAG	ATT	ATT	GAT	CTA	CTC	CCT	AAG	GTG	GAA	GTG	GCC	2640
	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys	Val	Glu	Val	Ala	
	865					870					875					880	
35	CTC	AGT	AAT	ATC	AAA	GAA	GCT	GAC	AAT	ACT	GTC	ATG	TTC	ATG	CAG	GGA	2688
	Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met	Phe	Met	Gln	Gly	
					885					890					895		
40	AAA	AGG	CAG	AAA	GAA	ATA	TGG	CAT	CTC	CTT	AAA	ATT	GCC	TGT	ACA	CAG	2736
	Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile	Ala	Cys	Thr	Gln	
				900					905					910			
45	AGT	TCT	GCC	CGC	TCT	CTT	GTA	GGA	TCC	AGT	CTA	GAA	GGT	GCA	GTA	ACC	2784
	Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu	Gly	Ala	Val	Thr	
			915					920						925			
50	CCT	CAG	ACA	TCA	GCA	TGG	CTG	CCC	CCG	ACT	TCA	GCA	GAA	CAT	GAT	CAT	2832
	Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala	Glu	His	Asp	His	
			930				935					940					
55	TCT	CTG	TCA	TGT	GTG	GTA	ACT	CCT	CAA	GAT	GGG	GAG	ACT	TCA	GCA	CAA	2880
	Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu	Thr	Ser	Ala	Gln	
	945					950					955					960	
60	ATG	ATA	GAA	GAA	AAT	TTG	AAC	TGC	CTT	GGC	CAT	TTA	AGC	ACT	ATT	ATT	2928
	Met	Ile	Glu	Glu	Asn	Leu	Asn	Cys	Leu	Gly	His	Leu	Ser	Thr	Ile	Ile	
					965					970					975		
65	CAT	GAG	GCA	AAT	GAG	GAA	CAG	GGC	AAT	AGT	ATG	ATG	AAT	CTT	GAT	TGG	2976
	His	Glu	Ala	Asn	Glu	Glu	Gln	Gly	Asn	Ser	Met	Met	Asn	Leu	Asp	Trp	
				980					985					990			
70	AGT	TGG	TTA	ACA	GAA	TGA											2994

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Ser Trp Leu Thr Glu
995

5 (2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 amino acids
(B) TYPE: amino acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35					40					45			
25	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55						60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75					80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
35	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135						140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155				160		
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165					170				175			
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195			200						205				
45	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210					215					220						
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235				240		
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Glu	Arg	Pro	
					245					250				255			
50	Pro	Gly	Leu	Arg	Pro	Gly	Ala	Gly	Gly	Pro	Trp	Glu	Met	Arg	Glu	Arg	
				260				265						270			
	Leu	Gly	Thr	Gly	Gly	Phe	Gly	Asn	Val	Cys	Leu	Tyr	Gln	His	Arg	Glu	
				275			280						285				
	Leu	Asp	Leu	Lys	Ile	Ala	Ile	Lys	Ser	Cys	Arg	Leu	Glu	Leu	Ser	Thr	
55		290				295					300						
	Lys	Asn	Arg	Glu	Arg	Trp	Cys	His	Glu	Ile	Gln	Ile	Met	Lys	Lys	Leu	

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	305		310		315		320
	Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro Glu Glu Leu Asn						
		325		330			335
5	Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu Tyr Cys Ser Gly						
		340		345			350
	Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn Cys Cys Gly Leu						
		355		360			365
	Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile Gly Ser Gly Ile						
		370		375			380
10	Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp Leu Lys Pro Glu						
		385		390			400
	Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile His Lys Ile Ile						
		405		410			415
	Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser Leu Cys Thr Ser						
15		420		425			430
	Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu Phe Glu Asn Lys						
		435		440			445
	Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly Thr Met Val Phe						
		450		455			460
20	Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His Leu Gln Pro Phe						
		465		470			480
	Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys Cys Ile Phe Ala						
		485		490			495
	Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser His Leu Pro Gln						
25		500		505			510
	Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met Glu Asn Trp Leu						
		515		520			525
	Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly Gly Pro Val Asp						
		530		535			540
30	Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met Asp His Ile Leu						
		545		550			560
	Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser Ala Lys Ile Ile						
		565		570			575
	Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser Leu Gln Ser Arg						
35		580		585			590
	Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln Glu Leu Leu Ser						
		595		600			605
	Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala Ser Gln Cys Val						
		610		615			620
40	Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val Tyr Leu Phe Asp						
		625		630			640
	Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser Arg Ser Leu Ser						
		645		650			655
	Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile Gln Leu Pro Ile						
45		660		665			670
	Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His Tyr Val Ser Gly						
		675		680			685
	Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln Arg Ala Ala Met						
		690		695			700
50	Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys Met Lys Asn Thr						
		705		710			720
	Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu Glu Phe Phe His						
		725		730			735
	Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu Gln Met Thr Tyr						
55		740		745			750
	Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys Glu Met Glu Glu						

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		755				760				765						
	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly	Tyr	Leu	Glu	Asp
		770					775					780				
5	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Gly	Leu	Gln	Lys	Ser	Pro
	785					790					795				800	
	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu	Glu	Gln	Arg	Ala
					805					810					815	
	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser	Asp	His	Ser	Tyr
					820				825					830		
10	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His	Thr	Val	Gln	Ser
		835						840				845				
	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu	Ser	Lys	Leu	Leu
		850					855					860				
15	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys	Val	Glu	Val	Ala
	865					870					875				880	
	Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met	Phe	Met	Gln	Gly
					885					890					895	
	Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile	Ala	Cys	Thr	Gln
					900				905					910		
20	Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu	Gly	Ala	Val	Thr
					915				920					925		
	Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala	Glu	His	Asp	His
					930			935				940				
	Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu	Thr	Ser	Ala	Gln
25	945					950					955				960	
	Met	Ile	Glu	Glu	Asn	Leu	Asn	Cys	Leu	Gly	His	Leu	Ser	Thr	Ile	Ile
					965					970					975	
	His	Glu	Ala	Asn	Glu	Glu	Gln	Gly	Asn	Ser	Met	Met	Asn	Leu	Asp	Trp
					980				985					990		
30	Ser	Trp	Leu	Thr	Glu											
					995											

(2) INFORMATION FOR SEQ ID NO:122:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2991 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2988
 - (D) OTHER INFORMATION:
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

50	ATG GAG CGG CCC CCG GGG CTG CGG CCG GGC GCG GGC GGG CCC TGG GAG	48
	Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu	
	1 5 10 15	
55	ATG CGG GAG CGG CTG GGC ACC GGC GGC TTC GGG AAC GTC TGT CTG TAC	96
	Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr	
	20 25 30	

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	CAG CAT CGG GAA CTT GAT CTC AAA ATA GCA ATT AAG TCT TGT CGC CTA	144
	Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu	
	35 40 45	
5	GAG CTA AGT ACC AAA AAC AGA GAA CGA TGG TGC CAT GAA ATC CAG ATT	192
	Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile	
	50 55 60	
10	ATG AAG AAG TTG AAC CAT GCC AAT GTT GTA AAG GCC TGT GAT GTT CCT	240
	Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro	
	65 70 75 80	
15	GAA GAA TTG AAT ATT TTG ATT CAT GAT GTG CCT CTT CTA GCA ATG GAA	288
	Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu	
	85 90 95	
20	TAC TGT TCT GGA GGA GAT CTC CGA AAG CTG CTC AAC AAA CCA GAA AAT	336
	Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn	
	100 105 110	
25	TGT TGT GGA CTT AAA GAA AGC CAG ATA CTT TCT TTA CTA AGT GAT ATA	384
	Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile	
	115 120 125	
30	GGG TCT GGG ATT CGA TAT TTG CAT GAA AAC AAA ATT ATA CAT CGA GAT	432
	Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp	
	130 135 140	
35	CTA AAA CCT GAA AAC ATA GTT CTT CAG GAT GTT GGT GGA AAG ATA ATA	480
	Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile	
	145 150 155 160	
40	CAT AAA ATA ATT GAT CTG GGA TAT GCC AAA GAT GTT GAT CAA GGA AGT	528
	His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser	
	165 170 175	
45	CTG TGT ACA TCT TTT GTG GGA ACA CTG CAG TAT CTG GCC CCA GAG CTC	576
	Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu	
	180 185 190	
50	TTT GAG AAT AAG CCT TAC ACA GCC ACT GTT GAT TAT TGG AGC TTT GGG	624
	Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly	
	195 200 205	
55	ACC ATG GTA TTT GAA TGT ATT GCT GGA TAT AGG CCT TTT TTG CAT CAT	672
	Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His	
	210 215 220	
60	CTG CAG CCA TTT ACC TGG CAT GAG AAG ATT AAG AAG AAG GAT CCA AAG	720
	Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys	
	225 230 235 240	
65	TGT ATA TTT GCA TGT GAA GAG ATG TCA GGA GAA GTT CGG TTT AGT AGC	768
	Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser	
	245 250 255	

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235

	CAT TTA CCT CAA CCA AAT AGC CTT TGT AGT TTA ATA GTA GAA CCC ATG	816
	His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met	
	260 265 270	
5	GAA AAC TGG CTA CAG TTG ATG TTG AAT TGG GAC CCT CAG CAG AGA GGA	864
	Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly	
	275 280 285	
10	GGA CCT GTT GAC CTT ACT TTG AAG CAG CCA AGA TGT TTT GTA TTA ATG	912
	Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met	
	290 295 300	
15	GAT CAC ATT TTG AAT TTG AAG ATA GTA CAC ATC CTA AAT ATG ACT TCT	960
	Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser	
	305 310 315 320	
20	GCA AAG ATA ATT TCT TTT CTG TTA CCA CCT GAT GAA AGT CTT CAT TCA	1008
	Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser	
	325 330 335	
25	CTA CAG TCT CGT ATT GAG CGT GAA ACT GGA ATA AAT ACT GGT TCT CAA	1056
	Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln	
	340 345 350	
30	GAA CTT CTT TCA GAG ACA GGA ATT TCT CTG GAT CCT CGG AAA CCA GCC	1104
	Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala	
	355 360 365	
35	TCT CAA TGT GTT CTA GAT GGA GTT AGA GGC TGT GAT AGC TAT ATG GTT	1152
	Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val	
	370 375 380	
40	TAT TTG TTT GAT AAA AGT AAA ACT GTA TAT GAA GGG CCA TTT GCT TCC	1200
	Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser	
	385 390 395 400	
45	AGA AGT TTA TCT GAT TGT GTA AAT TAT ATT GTA CAG GAC AGC AAA ATA	1248
	Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile	
	405 410 415	
50	CAG CTT CCA ATT ATA CAG CTG CGT AAA GTG TGG GCT GAA GCA GTG CAC	1296
	Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His	
	420 425 430	
55	TAT GTG TCT GGA CTA AAA GAA GAC TAT AGC AGG CTC TTT CAG GGA CAA	1344
	Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln	
	435 440 445	
60	AGG GCA GCA ATG TTA AGT CTT CTT AGA TAT AAT GCT AAC TTA ACA AAA	1392
	Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys	
	450 455 460	
65	ATG AAG AAC ACT TTG ATC TCA GCA TCA CAA CAA CTG AAA GCT AAA TTG	1440
	Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu	
	465 470 475 480	

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236

	GAG TTT TTT CAC AAA AGC ATT CAG CTT GAC TTG GAG AGA TAC AGC GAG	1488
	Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu	
	485 490 495	
5	CAG ATG ACG TAT GGG ATA TCT TCA GAA AAA ATG CTA AAA GCA TGG AAA	1536
	Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys	
	500 505 510	
10	GAA ATG GAA GAA AAG GCC ATC CAC TAT GCT GAG GTT GGT GTC ATT GGA	1584
	Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly	
	515 520 525	
15	TAC CTG GAG GAT CAG ATT ATG TCT TTG CAT GCT GAA ATC ATG GGG CTA	1632
	Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu	
	530 535 540	
20	CAG AAG AGC CCC TAT GGA AGA CGT CAG GGA GAC TTG ATG GAA TCT CTG	1680
	Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu	
	545 550 555 560	
25	GAA CAG CGT GCC ATT GAT CTA TAT AAG CAG TTA AAA CAC AGA CCT TCA	1728
	Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser	
	565 570 575	
30	GAT CAC TCC TAC AGT GAC AGC ACA GAG ATG GTG AAA ATC ATT GTG CAC	1776
	Asp His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His	
	580 585 590	
35	ACT GTG CAG AGT CAG GAC CGT GTG CTC AAG GAG CTG TTT GGT CAT TTG	1824
	Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu	
	595 600 605	
40	AGC AAG TTG TTG GGC TGT AAG CAG AAG ATT ATT GAT CTA CTC CCT AAG	1872
	Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys	
	610 615 620	
45	GTG GAA GTG GCC CTC AGT AAT ATC AAA GAA GCT GAC AAT ACT GTC ATG	1920
	Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met	
	625 630 635 640	
50	TTC ATG CAG GGA AAA AGG CAG AAA GAA ATA TGG CAT CTC CTT AAA ATT	1968
	Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile	
	645 650 655	
55	GCC TGT ACA CAG AGT TCT GCC CGC TCT CTT GTA GGA TCC AGT CTA GAA	2016
	Ala Cys Thr Gln Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu	
	660 665 670	
60	GGT GCA GTA ACC CCT CAG ACA TCA GCA TGG CTG CCC CCG ACT TCA GCA	2064
	Gly Ala Val Thr Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala	
	675 680 685	
65	GAA CAT GAT CAT TCT CTG TCA TGT GTG GTA ACT CCT CAA GAT GGG GAG	2112
	Glu His Asp His Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu	
	690 695 700	

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5	ACT TCA GCA CAA ATG ATA GAA GAA AAT TTG AAC TGC CTT GGC CAT TTA	2160
	Thr Ser Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu	
	705 710 715 720	
	AGC ACT ATT ATT CAT GAG GCA AAT GAG GAA CAG GGC AAT AGT ATG ATG	2208
	Ser Thr Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met	
10	725 730 735	
	AAT CTT GAT TGG AGT TGG TTA ACA GAA TGG GTA CCG CGG GCC CGG GAT	2256
	Asn Leu Asp Trp Ser Trp Leu Thr Glu Trp Val Pro Arg Ala Arg Asp	
	740 745 750	
	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG	2304
15	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly	
	755 760 765	
	GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG	2352
	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys	
	770 775 780	
20	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG	2400
	Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu	
	785 790 795 800	
	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC	2448
	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro	
25	805 810 815	
	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC	2496
	Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr	
	820 825 830	
	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA	2544
30	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	
	835 840 845	
	GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC	2592
	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr	
	850 855 860	
35	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC	2640
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	
	865 870 875 880	
	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG	2688
	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly	
40	885 890 895	
	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC	2736
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala	
	900 905 910	
	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC	2784
45	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
	915 920 925	
50		
55		

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	ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC	2832
	Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr	
	930 935 940	
5	CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC	2880
	Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser	
	945 950 955 960	
10	ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG	2928
	Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met	
	965 970 975	
15	GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC	2976
	Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp	
	980 985 990	
	GAG CTG TAC AAG TAA	2991
20	Glu Leu Tyr Lys	
	995	

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 996 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

35	Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu	
	1 5 10 15	
	Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr	
	20 25 30	
40	Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu	
	35 40 45	
	Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile	
	50 55 60	
45	Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro	
	65 70 75 80	
	Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu	
	85 90 95	
	Tyr Cys Ser Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn	
	100 105 110	
50	Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile	
	115 120 125	
	Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp	
	130 135 140	
	Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile	
55	145 150 155 160	
	His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser	

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					165					170					175	
	Leu	Cys	Thr	Ser	Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu
				180					185					190		
5	Phe	Glu	Asn	Lys	Pro	Tyr	Thr	Ala	Thr	Val	Asp	Tyr	Trp	Ser	Phe	Gly
			195					200					205			
	Thr	Met	Val	Phe	Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His
		210					215				220					
	Leu	Gln	Pro	Phe	Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys
	225					230					235				240	
10	Cys	Ile	Phe	Ala	Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser
				245					250					255		
	His	Leu	Pro	Gln	Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met
			260						265				270			
15	Glu	Asn	Trp	Leu	Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly
		275						280				285				
	Gly	Pro	Val	Asp	Leu	Thr	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met
		290					295				300					
	Asp	His	Ile	Leu	Asn	Leu	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser
	305					310					315				320	
20	Ala	Lys	Ile	Ile	Ser	Phe	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser
				325					330					335		
	Leu	Gln	Ser	Arg	Ile	Glu	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln
			340					345				350				
25	Glu	Leu	Leu	Ser	Glu	Thr	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala
		355					360				365					
	Ser	Gln	Cys	Val	Leu	Asp	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Val
		370					375				380					
	Tyr	Leu	Phe	Asp	Lys	Ser	Lys	Thr	Val	Tyr	Glu	Gly	Pro	Phe	Ala	Ser
	385					390				395					400	
30	Arg	Ser	Leu	Ser	Asp	Cys	Val	Asn	Tyr	Ile	Val	Gln	Asp	Ser	Lys	Ile
				405					410					415		
	Gln	Leu	Pro	Ile	Ile	Gln	Leu	Arg	Lys	Val	Trp	Ala	Glu	Ala	Val	His
			420					425				430				
35	Tyr	Val	Ser	Gly	Leu	Lys	Glu	Asp	Tyr	Ser	Arg	Leu	Phe	Gln	Gly	Gln
		435					440				445					
	Arg	Ala	Ala	Met	Leu	Ser	Leu	Leu	Arg	Tyr	Asn	Ala	Asn	Leu	Thr	Lys
		450					455				460					
	Met	Lys	Asn	Thr	Leu	Ile	Ser	Ala	Ser	Gln	Gln	Leu	Lys	Ala	Lys	Leu
	465				470				475					480		
40	Glu	Phe	Phe	His	Lys	Ser	Ile	Gln	Leu	Asp	Leu	Glu	Arg	Tyr	Ser	Glu
				485					490					495		
	Gln	Met	Thr	Tyr	Gly	Ile	Ser	Ser	Glu	Lys	Met	Leu	Lys	Ala	Trp	Lys
		500						505				510				
45	Glu	Met	Glu	Glu	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly
		515					520				525					
	Tyr	Leu	Glu	Asp	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Gly	Leu
		530					535				540					
	Gln	Lys	Ser	Pro	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu
	545					550				555					560	
50	Glu	Gln	Arg	Ala	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser
				565					570					575		
	Asp	His	Ser	Tyr	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His
			580					585				590				
55	Thr	Val	Gln	Ser	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu
		595					600				605					
	Ser	Lys	Leu	Leu	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys

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	610		615		620														
	Val	Glu	Val	Ala	Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met			
	625						630				635					640			
5	Phe	Met	Gln	Gly	Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile			
					645				650						655				
	Ala	Cys	Thr	Gln	Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu			
				660					665					670					
	Gly	Ala	Val	Thr	Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala			
			675					680					685						
10	Glu	His	Asp	His	Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu			
		690					695					700							
	Thr	Ser	Ala	Gln	Met	Ile	Glu	Glu	Asn	Leu	Asn	Cys	Leu	Gly	His	Leu			
	705					710			715						720				
	Ser	Thr	Ile	Ile	His	Glu	Ala	Asn	Glu	Gln	Gly	Asn	Ser	Met	Met				
15					725				730					735					
	Asn	Leu	Asp	Trp	Ser	Trp	Leu	Thr	Glu	Trp	Val	Pro	Arg	Ala	Arg	Asp			
			740					745				750							
	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly			
		755					760					765							
20	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys			
		770					775				780								
	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu			
	785				790				795						800				
	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro			
25					805				810					815					
	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr			
			820				825					830							
	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu			
		835					840					845							
30	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr			
		850				855					860								
	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg			
	865				870				875						880				
	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly			
35					885				890					895					
	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala			
			900				905					910							
	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn			
		915					920					925							
40	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr			
		930				935						940							
	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser			
	945				950				955						960				
	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met			
45					965				970					975					
	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp			
			980				985						990						
	Glu	Leu	Tyr	Lys															
			995																

50

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

240

241

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1905

(D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

15	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
20	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
25	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
30	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
35	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
40	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
45	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
50	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
60	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
65	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
70	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576

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242

	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
5	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
10	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215				220						
15	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235						240	
20	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCC	ATG	AGC	GAG	ACG	GTC	ATC	ATG	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ser	Glu	Thr	Val	Ile	Met	
					245				250						255		
25	AGC	GAG	ACG	GTC	ATC	TGT	TCC	AGC	CGG	GCC	ACT	GTG	ATG	CTT	TAT	GAT	816
	Ser	Glu	Thr	Val	Ile	Cys	Ser	Ser	Arg	Ala	Thr	Val	Met	Leu	Tyr	Asp	
			260					265					270				
30	GAT	GGC	AAC	AAG	CGA	TGG	CTC	CCT	GCT	GGC	ACG	GGT	CCC	CAG	GCC	TTC	864
	Asp	Gly	Asn	Lys	Arg	Trp	Leu	Pro	Ala	Gly	Thr	Gly	Pro	Gln	Ala	Phe	
		275					280					285					
35	AGC	CGC	GTC	CAG	ATC	TAC	CAC	AAC	CCC	ACG	GCC	AAT	TCC	TTT	CGC	GTC	912
	Ser	Arg	Val	Gln	Ile	Tyr	His	Asn	Pro	Thr	Ala	Asn	Ser	Phe	Arg	Val	
		290				295					300						
40	GTG	GGC	CGG	AAG	ATG	CAG	CCC	GAC	CAG	CAG	GTG	GTC	ATC	AAC	TGT	GCC	960
	Val	Gly	Arg	Lys	Met	Gln	Pro	Asp	Gln	Gln	Val	Val	Ile	Asn	Cys	Ala	
	305					310				315					320		
45	ATC	GTC	CGG	GGT	GTC	AAG	TAT	AAC	CAG	GCC	ACC	CCC	AAC	TTC	CAT	CAG	1008
	Ile	Val	Arg	Gly	Val	Lys	Tyr	Asn	Gln	Ala	Thr	Pro	Asn	Phe	His	Gln	
				325				330					335				
50	TGG	CGC	GAC	GCT	CGC	CAG	GTC	TGG	GGC	CTC	AAC	TTC	GGC	AGC	AAG	GAG	1056
	Trp	Arg	Asp	Ala	Arg	Gln	Val	Trp	Gly	Leu	Asn	Phe	Gly	Ser	Lys	Glu	
			340				345					350					
55	GAT	GGC	GCC	CAG	TTT	GCC	GCC	GGC	ATG	GCC	AGT	GCC	CTA	GAG	GCG	TTG	1104
	Asp	Ala	Ala	Gln	Phe	Ala	Ala	Gly	Met	Ala	Ser	Ala	Leu	Glu	Ala	Leu	
		355				360						365					
60	GAA	GGA	GGT	GGG	CCC	CCT	CCA	CCC	CCA	GCA	CTT	CCC	ACC	TGG	TCG	GTC	1152
	Glu	Gly	Gly	Gly	Pro	Pro	Pro	Pro	Pro	Ala	Leu	Pro	Thr	Trp	Ser	Val	
		370				375					380						
65	CCG	AAC	GGC	CCC	TCC	CCG	GAG	GAG	GTG	GAG	CAG	CAG	AAA	AGG	CAG	CAG	1200
	Pro	Asn	Gly	Pro	Ser	Pro	Glu	Glu	Val	Glu	Gln	Gln	Lys	Arg	Gln	Gln	
		385				390				395					400		
70	CCC	GGC	CCG	TCG	GAG	CAC	ATA	GAG	CGC	CGG	GTC	TCC	AAT	GCA	GGA	GGC	1248

242

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	Pro	Gly	Pro	Ser	Glu	His	Ile	Glu	Arg	Arg	Val	Ser	Asn	Ala	Gly	Gly	
					405					410					415		
5	CCA	CCT	GCT	CCC	CCC	GCT	GGG	GGT	CCA	CCC	CCA	CCA	CCA	GGA	CCT	CCC	1296
	Pro	Pro	Ala	Pro	Pro	Ala	Gly	Gly	Pro	Pro	Pro	Pro	Pro	Gly	Pro	Pro	
				420					425					430			
10	CCT	CCT	CCA	GGT	CCC	CCC	CCA	CCC	CCA	GGT	TTG	CCC	CCT	TCG	GGG	GTC	1344
	Pro	Pro	Pro	Gly	Pro	Pro	Pro	Pro	Pro	Gly	Leu	Pro	Pro	Ser	Gly	Val	
			435					440					445				
15	CCA	GCT	GCA	GCG	CAC	GGA	GCA	GGG	GGA	GGA	CCA	CCC	CCT	GCA	CCC	CCT	1392
	Pro	Ala	Ala	Ala	His	Gly	Ala	Gly	Gly	Gly	Pro	Pro	Pro	Ala	Pro	Pro	
		450					455					460					
20	CTC	CCG	GCA	GCA	CAG	GGC	CCT	GGT	GGT	GGG	GGA	GCT	GGG	GCC	CCA	GGC	1440
	Leu	Pro	Ala	Ala	Gln	Gly	Pro	Gly	Gly	Gly	Gly	Ala	Gly	Ala	Pro	Gly	
	465					470				475						480	
25	CTG	GCC	GCA	GCT	ATT	GCT	GGA	GCC	AAA	CTC	AGG	AAA	GTC	AGC	AAG	CAG	1488
	Leu	Ala	Ala	Ala	Ile	Ala	Gly	Ala	Lys	Leu	Arg	Lys	Val	Ser	Lys	Gln	
					485					490						495	
30	GAG	GAG	GCC	TCA	GGG	GGG	CCC	ACA	GCC	CCC	AAA	GCT	GAG	AGT	GGT	CGA	1536
	Glu	Glu	Ala	Ser	Gly	Gly	Pro	Thr	Ala	Pro	Lys	Ala	Glu	Ser	Gly	Arg	
			500						505					510			
35	AGC	GGA	GGT	GGG	GGA	CTC	ATG	GAA	GAG	ATG	AAC	GCC	ATG	CTG	GCC	CGG	1584
	Ser	Gly	Gly	Gly	Gly	Leu	Met	Glu	Glu	Met	Asn	Ala	Met	Leu	Ala	Arg	
			515					520					525				
40	AGA	AGG	AAA	GCC	ACG	CAA	GTT	GGG	GAG	AAA	ACC	CCC	AAG	GAT	GAA	TCT	1632
	Arg	Arg	Lys	Ala	Thr	Gln	Val	Gly	Glu	Lys	Thr	Pro	Lys	Asp	Glu	Ser	
		530					535					540					
45	GCC	AAT	CAG	GAG	GAG	CCA	GAG	GCC	AGA	GTC	CCG	GCC	CAG	AGT	GAA	TCT	1680
	Ala	Asn	Gln	Glu	Glu	Pro	Glu	Ala	Arg	Val	Pro	Ala	Gln	Ser	Glu	Ser	
	545					550				555					560		
50	GTG	CGG	AGA	CCC	TGG	GAG	AAG	AAC	AGC	ACA	ACC	TTG	CCA	AGG	ATG	AAG	1728
	Val	Arg	Arg	Pro	Trp	Glu	Lys	Asn	Ser	Thr	Thr	Leu	Pro	Arg	Met	Lys	
				565					570						575		
55	TCG	TCT	TCT	TCG	GTG	ACC	ACT	TCC	GAG	ACC	CAA	CCC	TGC	ACG	CCC	AGC	1776
	Ser	Ser	Ser	Ser	Val	Thr	Thr	Ser	Glu	Thr	Gln	Pro	Cys	Thr	Pro	Ser	
				580					585					590			
60	TCC	AGT	GAT	TAC	TCG	GAC	CTA	CAG	AGG	GTG	AAA	CAG	GAG	CTT	CTG	GAA	1824
	Ser	Ser	Asp	Tyr	Ser	Asp	Leu	Gln	Arg	Val	Lys	Gln	Glu	Leu	Leu	Glu	
			595				600					605					
65	GAG	GTG	AAG	AAG	GAA	TTG	CAG	AAA	GTG	AAA	GAG	GAA	ATC	ATT	GAA	GCC	1872
	Glu	Val	Lys	Lys	Glu	Leu	Gln	Lys	Val	Lys	Glu	Glu	Ile	Ile	Glu	Ala	
		610					615					620					
70	TTC	GTC	CAG	GAG	CTG	AGG	AAG	CGG	GGT	TCT	CCC	TGA					1908

243

244

Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro
 625 630 635

5 (2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 20 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 25 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 30 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 35 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 40 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 45 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met
 245 250 255
 50 Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp
 260 265 270
 Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe
 275 280 285
 Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val
 290 295 300
 55 Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala

244

245

	305		310		315		320
	Ile	Val	Arg	Gly	Val	Lys	Tyr
				325			330
	Trp	Arg	Asp	Ala	Arg	Gln	Val
5				340			345
	Asp	Ala	Ala	Gln	Phe	Ala	Ala
				355			360
	Glu	Gly	Gly	Gly	Pro	Pro	Pro
				370			375
10	Pro	Asn	Gly	Pro	Ser	Pro	Glu
				385			390
	Pro	Gly	Pro	Ser	Glu	His	Ile
				405			410
	Pro	Pro	Ala	Pro	Pro	Ala	Gly
15				420			425
	Pro	Pro	Pro	Gly	Pro	Pro	Pro
				435			440
	Pro	Ala	Ala	Ala	His	Gly	Ala
				450			455
20	Leu	Pro	Ala	Ala	Gln	Gly	Pro
				465			470
	Leu	Ala	Ala	Ala	Ile	Ala	Gly
				485			490
	Glu	Glu	Ala	Ser	Gly	Gly	Pro
25				500			505
	Ser	Gly	Gly	Gly	Gly	Leu	Met
				515			520
	Arg	Arg	Lys	Ala	Thr	Gln	Val
				530			535
30	Ala	Asn	Gln	Glu	Glu	Pro	Glu
				545			550
	Val	Arg	Arg	Pro	Trp	Glu	Lys
				565			570
	Ser	Ser	Ser	Ser	Val	Thr	Thr
35				580			585
	Ser	Ser	Asp	Tyr	Ser	Asp	Leu
				595			600
	Glu	Val	Lys	Lys	Glu	Leu	Gln
				610			615
40	Phe	Val	Gln	Glu	Leu	Arg	Lys
				625			630
							635

(2) INFORMATION FOR SEQ ID NO:126:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1326
 - (D) OTHER INFORMATION:
- 55

245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

5	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	48
10	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30	96
15	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45	144
20	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240
30	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288
35	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
60	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
65	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
70	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672

247

	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210						215					220					
5	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235						240	
10	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCA	ATG	GCT	GCC	ATC	CGG	AAG	AAA	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ala	Ala	Ile	Arg	Lys	Lys	
					245					250					255		
15	CTG	GTG	ATT	GTT	GGT	GAT	GGA	GCC	TGT	GGA	AAG	ACA	TGC	TTG	CTC	ATA	816
	Leu	Val	Ile	Val	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	
				260					265					270			
	GTC	TTC	AGC	AAG	GAC	CAG	TTC	CCA	GAG	GTG	TAT	GTG	CCC	ACA	GTG	TTT	864
	Val	Phe	Ser	Lys	Asp	Gln	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	
			275					280						285			
20	GAG	AAC	TAT	GTG	GCA	GAT	ATC	GAG	GTG	GAT	GGA	AAG	CAG	GTA	GAG	TTG	912
	Glu	Asn	Tyr	Val	Ala	Asp	Ile	Glu	Val	Asp	Gly	Lys	Gln	Val	Glu	Leu	
		290					295					300					
25	GCT	TTG	TGG	GAC	ACA	GCT	GGG	CAG	GAA	GAT	TAT	GAT	CGC	CTG	AGG	CCC	960
	Ala	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	
	305					310					315					320	
30	CTC	TCC	TAC	CCA	GAT	ACC	GAT	GTT	ATA	CTG	ATG	TGT	TTT	TCC	ATC	GAC	1008
	Leu	Ser	Tyr	Pro	Asp	Thr	Asp	Val	Ile	Leu	Met	Cys	Phe	Ser	Ile	Asp	
					325					330					335		
35	AGC	CCT	GAT	AGT	TTA	GAA	AAC	ATC	CCA	GAA	AAG	TGG	ACC	CCA	GAA	GTC	1056
	Ser	Pro	Asp	Ser	Leu	Glu	Asn	Ile	Pro	Glu	Lys	Trp	Thr	Pro	Glu	Val	
				340					345					350			
	AAG	CAT	TTC	TGT	CCC	AAC	GTG	CCC	ATC	ATC	CTG	GTT	GGG	AAT	AAG	AAG	1104
	Lys	His	Phe	Cys	Pro	Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Lys	
			355				360						365				
40	GAT	CTT	CGG	AAT	GAT	GAG	CAC	ACA	AGG	CGG	GAG	CTA	GCC	AAG	ATG	AAG	1152
	Asp	Leu	Arg	Asn	Asp	Glu	His	Thr	Arg	Arg	Glu	Leu	Ala	Lys	Met	Lys	
		370					375					380					
45	CAG	GAG	CCG	GTG	AAA	CCT	GAA	GAA	GGC	AGA	GAT	ATG	GCA	AAC	AGG	ATT	1200
	Gln	Glu	Pro	Val	Lys	Pro	Glu	Glu	Gly	Arg	Asp	Met	Ala	Asn	Arg	Ile	
	385					390					395					400	
50	GGC	GCT	TTT	GGG	TAC	ATG	GAG	TGT	TCA	GCA	AAG	ACC	AAA	GAT	GGA	GTG	1248
	Gly	Ala	Phe	Gly	Tyr	Met	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Asp	Gly	Val	
				405						410					415		
55	AGA	GAG	GTT	TTT	GAA	ATG	GCT	ACG	AGA	GCT	GCT	CTG	CAA	GCT	AGA	CGT	1296
	Arg	Glu	Val	Phe	Glu	Met	Ala	Thr	Arg	Ala	Ala	Leu	Gln	Ala	Arg	Arg	
				420					425					430			
	GGG	AAG	AAA	AAA	TCT	GGT	TGC	CTT	GTC	TTG	TGA						1329
																	247

248

Gly Lys Lys Lys Ser Gly Cys Leu Val Leu
435 440

5 (2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35				40					45				
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
25		50					55					60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75						80	
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
35		130					135					140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195			200						205				
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
45		210					215					220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ala	Ala	Ile	Arg	Lys	Lys	
					245				250						255		
50	Leu	Val	Ile	Val	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	
				260				265						270			
	Val	Phe	Ser	Lys	Asp	Gln	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	
				275				280					285				
	Glu	Asn	Tyr	Val	Ala	Asp	Ile	Glu	Val	Asp	Gly	Lys	Gln	Val	Glu	Leu	
55		290					295					300					
	Ala	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	

248

249

	305				310					315					320	
	Leu	Ser	Tyr	Pro	Asp	Thr	Asp	Val	Ile	Leu	Met	Cys	Phe	Ser	Ile	Asp
					325					330					335	
5	Ser	Pro	Asp	Ser	Leu	Glu	Asn	Ile	Pro	Glu	Lys	Trp	Thr	Pro	Glu	Val
				340					345					350		
	Lys	His	Phe	Cys	Pro	Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Lys
			355					360					365			
	Asp	Leu	Arg	Asn	Asp	Glu	His	Thr	Arg	Arg	Glu	Leu	Ala	Lys	Met	Lys
		370					375					380				
10	Gln	Glu	Pro	Val	Lys	Pro	Glu	Glu	Gly	Arg	Asp	Met	Ala	Asn	Arg	Ile
	385					390					395				400	
	Gly	Ala	Phe	Gly	Tyr	Met	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Asp	Gly	Val
				405						410				415		
	Arg	Glu	Val	Phe	Glu	Met	Ala	Thr	Arg	Ala	Ala	Leu	Gln	Ala	Arg	Arg
15				420					425					430		
	Gly	Lys	Lys	Lys	Ser	Gly	Cys	Leu	Val	Leu						
			435					440								

(2) INFORMATION FOR SEQ ID NO:128:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

30

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1137
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

35

ATG	GAC	CAT	TAT	GAT	TCT	CAG	CAA	ACC	AAC	GAT	TAC	ATG	CAG	CCA	GAA	48
Met	Asp	His	Tyr	Asp	Ser	Gln	Gln	Thr	Asn	Asp	Tyr	Met	Gln	Pro	Glu	
1				5					10					15		

40

GAG GAC TGG GAC CGG GAC CTG CTC CTG GAC CCG GCC TGG GAG AAG CAG 96
Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
20 25 30

45

CAG AGA AAG ACA TTC ACG GCA TGG TGT AAC TCC CAC CTC CGG AAG GCG 144
Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
35 40 45

50

GGG ACA CAG ATC GAG AAC ATC GAA GAG GAC TTC CGG GAT GGC CTG AAG 192
Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
50 55 60

55

CTC	ATG	CTG	CTG	CTG	GAG	GTC	ATC	TCA	GGT	GAA	CGC	TTG	GCC	AAG	CCA	240
Leu	Met	Leu	Leu	Leu	Glu	Val	Ile	Ser	Gly	Glu	Arg	Leu	Ala	Lys	Pro	
65					70					75					80	

GAG CGA GGC AAG ATG AGA GTG CAC AAG ATC TCC AAC GTC AAC AAG GCC 288

249

250

	Glu	Arg	Gly	Lys	Met	Arg	Val	His	Lys	Ile	Ser	Asn	Val	Asn	Lys	Ala	
					85					90					95		
5	CTG	GAT	TTC	ATA	GCC	AGC	AAA	GGC	GTC	AAA	CTG	GTG	TCC	ATC	GGA	GCC	336
	Leu	Asp	Phe	Ile	Ala	Ser	Lys	Gly	Val	Lys	Leu	Val	Ser	Ile	Gly	Ala	
				100					105					110			
10	GAA	GAA	ATC	GTG	GAT	GGG	AAT	GTG	AAG	ATG	ACC	CTG	GGC	ATG	ATC	TGG	384
	Glu	Glu	Ile	Val	Asp	Gly	Asn	Val	Lys	Met	Thr	Leu	Gly	Met	Ile	Trp	
				115				120					125				
15	ACC	ATC	ATC	CTG	CGC	AGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	432
	Thr	Ile	Ile	Leu	Arg	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	
				130			135					140					
20	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	480
	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	
				145			150				155					160	
25	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	528
	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	
				165						170						175	
30	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	576
	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	
				180					185					190			
35	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	624
	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	
				195				200					205				
40	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	672
	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	
				210			215					220					
45	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	720
	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	
				225			230				235					240	
50	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	768
	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	
					245				250						255		
55	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	816
	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	
				260					265					270			
60	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	864
	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	
				275				280					285				
65	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	912
	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	
				290			295					300					
70	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	960

250

251

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 305 310 315 320
 5 GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG 1008
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 325 330 335
 10 CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC 1056
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 340 345 350
 AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC 1104
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 355 360 365
 15 GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 1140
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 370 375

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 amino acids
 25 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 30 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

35 Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
 1 5 10 15
 Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
 20 25 30
 Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
 35 40 45
 40 Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
 50 55 60
 Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro
 65 70 75 80
 45 Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala
 85 90 95
 Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
 100 105 110
 Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
 115 120 125
 50 Thr Ile Ile Leu Arg Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys
 130 135 140
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 145 150 155 160
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 165 170 175
 55 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly

251

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		180		185		190													
	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly			
			195					200					205						
5	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe			
		210					215					220							
	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe			
	225					230					235					240			
	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu			
				245					250						255				
10	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys			
				260					265					270					
	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser			
		275						280					285						
15	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val			
		290					295					300							
	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala			
	305					310					315					320			
	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu			
				325						330					335				
20	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro			
				340					345					350					
	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala			
		355					360					365							
25	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys								
		370					375												

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...3513
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

45	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	48
	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5				10					15			
	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
50				20				25					30				
	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45					
55	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192

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253

	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50						55					60					
5	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75					80		
10	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
15	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
20	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
25	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150				155						160	
30	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
35	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185					190				
	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195				200					205				
40	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
45	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235						240	
50	GGA	CTC	AGA	TCT	CGA	GCC	ATG	AAC	GCC	CCC	GAG	CGG	CAG	CCC	CAA	CCC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Met	Asn	Ala	Pro	Glu	Arg	Gln	Pro	Gln	Pro	
					245				250						255		
55	GAC	GGC	GGG	GAC	GCC	CCA	GGC	CAC	GAG	CCT	GGG	GGC	AGC	CCC	CAA	GAC	816
	Asp	Gly	Gly	Asp	Ala	Pro	Gly	His	Glu	Pro	Gly	Gly	Ser	Pro	Gln	Asp	
				260				265					270				
	GAG	CTT	GAC	TTC	TCC	ATC	CTC	TTC	GAC	TAT	GAG	TAT	TTG	AAT	CCG	AAC	864

253

254

	Glu	Leu	Asp	Phe	Ser	Ile	Leu	Phe	Asp	Tyr	Glu	Tyr	Leu	Asn	Pro	Asn	
			275					280					285				
5	GAA	GAA	GAG	CCG	AAT	GCA	CAT	AAG	GTC	GCC	AGC	CCA	CCC	TCC	GGA	CCC	912
	Glu	Glu	Glu	Pro	Asn	Ala	His	Lys	Val	Ala	Ser	Pro	Pro	Ser	Gly	Pro	
			290				295					300					
10	GCA	TAC	CCC	GAT	GAT	GTA	ATG	GAC	TAT	GGC	CTC	AAG	CCA	TAC	AGC	CCC	960
	Ala	Tyr	Pro	Asp	Asp	Val	Met	Asp	Tyr	Gly	Leu	Lys	Pro	Tyr	Ser	Pro	
	305					310					315					320	
15	CTT	GCT	AGT	CTC	TCT	GGC	GAG	CCC	CCC	GGC	CGA	TTC	GGA	GAG	CCG	GAT	1008
	Leu	Ala	Ser	Leu	Ser	Gly	Glu	Pro	Pro	Gly	Arg	Phe	Gly	Glu	Pro	Asp	
					325					330					335		
20	AGG	GTA	GGG	CCG	CAG	AAG	TTT	CTG	AGC	GCG	GCC	AAG	CCA	GCA	GGG	GCC	1056
	Arg	Val	Gly	Pro	Gln	Lys	Phe	Leu	Ser	Ala	Ala	Lys	Pro	Ala	Gly	Ala	
				340					345					350			
25	TCG	GGC	CTG	AGC	CCT	CGG	ATC	GAG	ATC	ACT	CCG	TCC	CAC	GAA	CTG	ATC	1104
	Ser	Gly	Leu	Ser	Pro	Arg	Ile	Glu	Ile	Thr	Pro	Ser	His	Glu	Leu	Ile	
			355					360					365				
30	CAG	GCA	GTG	GGG	CCC	CTC	CGC	ATG	AGA	GAC	GCG	GGC	CTC	CTG	GTG	GAG	1152
	Gln	Ala	Val	Gly	Pro	Leu	Arg	Met	Arg	Asp	Ala	Gly	Leu	Leu	Val	Glu	
		370					375					380					
35	CAG	CCT	CCC	CTG	GCC	GGG	GTG	GCC	GCC	AGC	CCG	AGG	TTC	ACC	CTG	CCC	1200
	Gln	Pro	Pro	Leu	Ala	Gly	Val	Ala	Ala	Ser	Pro	Arg	Phe	Thr	Leu	Pro	
	385					390					395					400	
40	GTG	CCC	GGC	TTC	GAG	GGC	TAC	CGC	GAG	CCG	CTT	TGC	TTG	AGC	CCC	GCT	1248
	Val	Pro	Gly	Phe	Glu	Gly	Tyr	Arg	Glu	Pro	Leu	Cys	Leu	Ser	Pro	Ala	
					405					410					415		
45	AGC	AGC	GGC	TCC	TCT	GCC	AGC	TTC	ATT	TCT	GAC	ACC	TTC	TCC	CCC	TAC	1296
	Ser	Ser	Gly	Ser	Ser	Ala	Ser	Phe	Ile	Ser	Asp	Thr	Phe	Ser	Pro	Tyr	
				420				425						430			
50	ACC	TCG	CCC	TGC	GTC	TCG	CCC	AAT	AAC	GGC	GGG	CCC	GAC	GAC	CTG	TGT	1344
	Thr	Ser	Pro	Cys	Val	Ser	Pro	Asn	Asn	Gly	Gly	Pro	Asp	Asp	Leu	Cys	
			435				440						445				
55	CCG	CAG	TTT	CAA	AAC	ATC	CCT	GCT	CAT	TAT	TCC	CCC	AGA	ACC	TCG	CCA	1392
	Pro	Gln	Phe	Gln	Asn	Ile	Pro	Ala	His	Tyr	Ser	Pro	Arg	Thr	Ser	Pro	
		450					455					460					
60	ATA	ATG	TCA	CCT	CGA	ACC	AGC	CTC	GCC	GAG	GAC	AGC	TGC	CTG	GGC	CGC	1440
	Ile	Met	Ser	Pro	Arg	Thr	Ser	Leu	Ala	Glu	Asp	Ser	Cys	Leu	Gly	Arg	
	465					470					475					480	
65	CAC	TCG	CCC	GTG	CCC	CGT	CCG	GCC	TCC	CGC	TCC	TCA	TCG	CCT	GGT	GCC	1488
	His	Ser	Pro	Val	Pro	Arg	Pro	Ala	Ser	Arg	Ser	Ser	Ser	Pro	Gly	Ala	
					485					490					495		
70	AAG	CGG	AGG	CAT	TCG	TGC	GCC	GAG	GCC	TTG	GTT	GCC	CTG	CCG	CCC	GGA	1536

254

255

	Lys	Arg	Arg	His	Ser	Cys	Ala	Glu	Ala	Leu	Val	Ala	Leu	Pro	Pro	Gly	
				500					505					510			
5	GCC	TCA	CCC	CAG	CGC	TCC	CGG	AGC	CCC	TCG	CCG	CAG	CCC	TCA	TCT	CAC	1584
	Ala	Ser	Pro	Gln	Arg	Ser	Arg	Ser	Pro	Ser	Pro	Gln	Pro	Ser	Ser	His	
			515				520					525					
10	GTG	GCA	CCC	CAG	GAC	CAC	GGC	TCC	CCG	GCT	GGG	TAC	CCC	CCT	GTG	GCT	1632
	Val	Ala	Pro	Gln	Asp	His	Gly	Ser	Pro	Ala	Gly	Tyr	Pro	Pro	Val	Ala	
			530				535					540					
15	GGC	TCT	GCC	GTG	ATC	ATG	GAT	GCC	CTG	AAC	AGC	CTC	GCC	ACG	GAC	TCG	1680
	Gly	Ser	Ala	Val	Ile	Met	Asp	Ala	Leu	Asn	Ser	Leu	Ala	Thr	Asp	Ser	
	545					550					555					560	
	CCT	TGT	GGG	ATC	CCC	CCC	AAG	ATG	TGG	AAG	ACC	AGC	CCT	GAC	CCC	TCG	1728
	Pro	Cys	Gly	Ile	Pro	Pro	Lys	Met	Trp	Lys	Thr	Ser	Pro	Asp	Pro	Ser	
				565					570						575		
20	CCG	GTG	TCT	GCC	GCC	CCA	TCC	AAG	GCC	GGC	CTG	CCT	CGC	CAC	ATC	TAC	1776
	Pro	Val	Ser	Ala	Ala	Pro	Ser	Lys	Ala	Gly	Leu	Pro	Arg	His	Ile	Tyr	
				580					585					590			
25	CCG	GCC	GTG	GAG	TTC	CTG	GGG	CCC	TGC	GAG	CAG	GGC	GAG	AGG	AGA	AAC	1824
	Pro	Ala	Val	Glu	Phe	Leu	Gly	Pro	Cys	Glu	Gln	Gly	Glu	Arg	Arg	Asn	
			595				600						605				
30	TCG	GCT	CCA	GAA	TCC	ATC	CTG	CTG	GTT	CCG	CCC	ACT	TGG	CCC	AAG	CCG	1872
	Ser	Ala	Pro	Glu	Ser	Ile	Leu	Leu	Val	Pro	Pro	Thr	Trp	Pro	Lys	Pro	
			610				615					620					
35	CTG	GTG	CCT	GCC	ATT	CCC	ATC	TGC	AGC	ATC	CCA	GTG	ACT	GCA	TCC	CTC	1920
	Leu	Val	Pro	Ala	Ile	Pro	Ile	Cys	Ser	Ile	Pro	Val	Thr	Ala	Ser	Leu	
	625					630					635					640	
	CCT	CCA	CTT	GAG	TGG	CCG	CTG	TCC	AGT	CAG	TCA	GGC	TCT	TAC	GAG	CTG	1968
	Pro	Pro	Leu	Glu	Trp	Pro	Leu	Ser	Ser	Gln	Ser	Gly	Ser	Tyr	Glu	Leu	
				645						650					655		
40	CGG	ATC	GAG	GTG	CAG	CCC	AAG	CCA	CAT	CAC	CGG	GCC	CAC	TAT	GAG	ACA	2016
	Arg	Ile	Glu	Val	Gln	Pro	Lys	Pro	His	His	Arg	Ala	His	Tyr	Glu	Thr	
				660					665					670			
45	GAA	GGC	AGC	CGA	GGG	GCT	GTC	AAA	GCT	CCA	ACT	GGA	GGC	CAC	CCT	GTG	2064
	Glu	Gly	Ser	Arg	Gly	Ala	Val	Lys	Ala	Pro	Thr	Gly	Gly	His	Pro	Val	
			675					680					685				
50	GTT	CAG	CTC	CAT	GGC	TAC	ATG	GAA	AAC	AAG	CCT	CTG	GGA	CTT	CAG	ATC	2112
	Val	Gln	Leu	His	Gly	Tyr	Met	Glu	Asn	Lys	Pro	Leu	Gly	Leu	Gln	Ile	
			690				695					700					
55	TTC	ATT	GGG	ACA	GCT	GAT	GAG	CGG	ATC	CTT	AAG	CCG	CAC	GCC	TTC	TAC	2160
	Phe	Ile	Gly	Thr	Ala	Asp	Glu	Arg	Ile	Leu	Lys	Pro	His	Ala	Phe	Tyr	
	705					710					715					720	
	CAG	GTG	CAC	CGA	ATC	ACG	GGG	AAA	ACT	GTC	ACC	ACC	ACC	AGC	TAT	GAG	2208

255

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	Gln	Val	His	Arg	Ile	Thr	Gly	Lys	Thr	Val	Thr	Thr	Thr	Ser	Tyr	Glu	
					725					730						735	
5	AAG	ATA	GTG	GGC	AAC	ACC	AAA	GTC	CTG	GAG	ATC	CCC	TTG	GAG	CCC	AAA	2256
	Lys	Ile	Val	Gly	Asn	Thr	Lys	Val	Leu	Glu	Ile	Pro	Leu	Glu	Pro	Lys	
				740				745					750				
10	AAC	AAC	ATG	AGG	GCA	ACC	ATC	GAC	TGT	GCG	GGG	ATC	TTG	AAG	CTT	AGA	2304
	Asn	Asn	Met	Arg	Ala	Thr	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Lys	Leu	Arg	
			755					760					765				
15	AAC	GCC	GAC	ATT	GAG	CTG	CGG	AAA	GGC	GAG	ACG	GAC	ATT	GGA	AGA	AAG	2352
	Asn	Ala	Asp	Ile	Glu	Leu	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	Arg	Lys	
		770					775					780					
20	AAC	ACG	CGG	GTG	AGA	CTG	GTT	TTC	CGA	GTT	CAC	ATC	CCA	GAG	TCC	AGT	2400
	Asn	Thr	Arg	Val	Arg	Leu	Val	Phe	Arg	Val	His	Ile	Pro	Glu	Ser	Ser	
	785					790					795					800	
25	GGC	AGA	ATC	GTC	TCT	TTA	CAG	ACT	GCA	TCT	AAC	CCC	ATC	GAG	TGC	TCC	2448
	Gly	Arg	Ile	Val	Ser	Leu	Gln	Thr	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	
				805						810					815		
30	CAG	CGA	TCT	GCT	CAC	GAG	CTG	CCC	ATG	GTT	GAA	AGA	CAA	GAC	ACA	GAC	2496
	Gln	Arg	Ser	Ala	His	Glu	Leu	Pro	Met	Val	Glu	Arg	Gln	Asp	Thr	Asp	
			820					825						830			
35	AGC	TGC	CTG	GTC	TAT	GGC	GGC	CAG	CAA	ATG	ATC	CTC	ACG	GGG	CAG	AAC	2544
	Ser	Cys	Leu	Val	Tyr	Gly	Gly	Gln	Gln	Met	Ile	Leu	Thr	Gly	Gln	Asn	
		835						840					845				
40	TTT	ACA	TCC	GAG	TCC	AAA	GTT	GTG	TTT	ACT	GAG	AAG	ACC	ACA	GAT	GGA	2592
	Phe	Thr	Ser	Glu	Ser	Lys	Val	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly	
		850					855					860					
45	CAG	CAA	ATT	TGG	GAG	ATG	GAA	GCC	ACG	GTG	GAT	AAG	GAC	AAG	AGC	CAG	2640
	Gln	Gln	Ile	Trp	Glu	Met	Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	
	865					870					875					880	
50	CCC	AAC	ATG	CTT	TTT	GTT	GAG	ATC	CCT	GAA	TAT	CGG	AAC	AAG	CAT	ATC	2688
	Pro	Asn	Met	Leu	Phe	Val	Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	
				885					890						895		
55	CGC	ACA	CCT	GTA	AAA	GTG	AAC	TTC	TAC	GTC	ATC	AAT	GGG	AAG	AGA	AAA	2736
	Arg	Thr	Pro	Val	Lys	Val	Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	
			900						905					910			
60	CGA	AGT	CAG	CCT	CAG	CAC	TTT	ACC	TAC	CAC	CCA	GTC	CCA	GCC	ATC	AAG	2784
	Arg	Ser	Gln	Pro	Gln	His	Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	
			915					920					925				
65	ACG	GAG	CCC	ACG	GAT	GAA	TAT	GAC	CCC	ACT	CTG	ATC	TGC	AGC	CCC	ACC	2832
	Thr	Glu	Pro	Thr	Asp	Glu	Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	
		930					935					940					
70	CAT	GGA	GGC	CTG	GGG	AGC	CAG	CCT	TAC	TAC	CCC	CAG	CAC	CCG	ATG	GTG	2880

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	His	Gly	Gly	Leu	Gly	Ser	Gln	Pro	Tyr	Tyr	Pro	Gln	His	Pro	Met	Val	
	945					950					955					960	
5	GCC	GAG	TCC	CCC	TCC	TGC	CTC	GTG	GCC	ACC	ATG	GCT	CCC	TGC	CAG	CAG	2928
	Ala	Glu	Ser	Pro	Ser	Cys	Leu	Val	Ala	Thr	Met	Ala	Pro	Cys	Gln	Gln	
					965					970					975		
10	TTC	CGC	ACG	GGG	CTC	TCA	TCC	CCT	GAC	GCC	CGC	TAC	CAG	CAA	CAG	AAC	2976
	Phe	Arg	Thr	Gly	Leu	Ser	Ser	Pro	Asp	Ala	Arg	Tyr	Gln	Gln	Gln	Asn	
				980					985					990			
15	CCA	GCG	GCC	GTA	CTC	TAC	CAG	CGG	AGC	AAG	AGC	CTG	AGC	CCC	AGC	CTG	3024
	Pro	Ala	Ala	Val	Leu	Tyr	Gln	Arg	Ser	Lys	Ser	Leu	Ser	Pro	Ser	Leu	
				995				1000						1005			
20	CTG	GGC	TAT	CAG	CAG	CCG	GCC	CTC	ATG	GCC	GCC	CCG	CTG	TCC	CTT	GCG	3072
	Leu	Gly	Tyr	Gln	Gln	Pro	Ala	Leu	Met	Ala	Ala	Pro	Leu	Ser	Leu	Ala	
		1010						1015					1020				
25	GAC	GCT	CAC	CGC	TCT	GTG	CTG	GTG	CAC	GCC	GGC	TCC	CAG	GGC	CAG	AGC	3120
	Asp	Ala	His	Arg	Ser	Val	Leu	Val	His	Ala	Gly	Ser	Gln	Gly	Gln	Ser	
	1025					1030					1035					1040	
30	TCA	GCC	CTG	CTC	CAC	CCC	TCT	CCG	ACC	AAC	CAG	CAG	GCC	TCG	CCT	GTG	3168
	Ser	Ala	Leu	Leu	His	Pro	Ser	Pro	Thr	Asn	Gln	Gln	Ala	Ser	Pro	Val	
					1045					1050					1055		
35	ATC	CAC	TAC	TCA	CCC	ACC	AAC	CAG	CAG	CTG	CGC	TGC	GGA	AGC	CAC	CAG	3216
	Ile	His	Tyr	Ser	Pro	Thr	Asn	Gln	Gln	Leu	Arg	Cys	Gly	Ser	His	Gln	
				1060						1065					1070		
40	GAG	TTC	CAG	CAC	ATC	ATG	TAC	TGC	GAG	AAT	TTC	GCA	CCA	GGC	ACC	ACC	3264
	Glu	Phe	Gln	His	Ile	Met	Tyr	Cys	Glu	Asn	Phe	Ala	Pro	Gly	Thr	Thr	
			1075						1080				1085				
45	AGA	CCT	GGC	CCG	CCC	CCG	GTC	AGT	CAA	GGT	CAG	AGG	CTG	AGC	CCG	GGT	3312
	Arg	Pro	Gly	Pro	Pro	Pro	Val	Ser	Gln	Gly	Gln	Arg	Leu	Ser	Pro	Gly	
			1090					1095					1100				
50	TCC	TAC	CCC	ACA	GTC	ATT	CAG	CAG	CAG	AAT	GCC	ACG	AGC	CAA	AGA	GCC	3360
	Ser	Tyr	Pro	Thr	Val	Ile	Gln	Gln	Gln	Asn	Ala	Thr	Ser	Gln	Arg	Ala	
	1105					1110					1115					1120	
55	GCC	AAA	AAC	GGA	CCC	CCG	GTC	AGT	GAC	CAA	AAG	GAA	GTA	TTA	CCT	GCG	3408
	Ala	Lys	Asn	Gly	Pro	Pro	Val	Ser	Asp	Gln	Lys	Glu	Val	Leu	Pro	Ala	
					1125					1130					1135		
60	GGG	GTG	ACC	ATT	AAA	CAG	GAG	CAG	AAC	TTG	GAC	CAG	ACC	TAC	TTG	GAT	3456
	Gly	Val	Thr	Ile	Lys	Gln	Glu	Gln	Asn	Leu	Asp	Gln	Thr	Tyr	Leu	Asp	
				1140					1145					1150			
65	GAT	GTT	AAT	GAA	ATT	ATC	AGG	AAG	GAG	TTT	TCA	GGA	CCT	CCT	GCC	AGA	3504
	Asp	Val	Asn	Glu	Ile	Ile	Arg	Lys	Glu	Phe	Ser	Gly	Pro	Pro	Ala	Arg	
				1155				1160						1165			
70	AAT	CAG	ACG	TAA													3516
																	257

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Asn Gln Thr
1170

5 (2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1171 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
	1				5					10					15	
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
				20					25					30		
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
			35					40					45			
25	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
	65				70					75					80	
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
				85						90					95	
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
				100					105					110		
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
			115					120					125			
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
35		130					135					140				
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	145					150					155				160	
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
				165					170					175		
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
				180					185					190		
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
			195				200						205			
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
45		210					215					220				
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
	225					230					235				240	
	Gly	Leu	Arg	Ser	Arg	Ala	Met	Asn	Ala	Pro	Glu	Arg	Gln	Pro	Gln	Pro
				245						250				255		
50	Asp	Gly	Gly	Asp	Ala	Pro	Gly	His	Glu	Pro	Gly	Gly	Ser	Pro	Gln	Asp
				260					265					270		
	Glu	Leu	Asp	Phe	Ser	Ile	Leu	Phe	Asp	Tyr	Glu	Tyr	Leu	Asn	Pro	Asn
		275						280					285			
	Glu	Glu	Glu	Pro	Asn	Ala	His	Lys	Val	Ala	Ser	Pro	Pro	Ser	Gly	Pro
55		290					295					300				
	Ala	Tyr	Pro	Asp	Asp	Val	Met	Asp	Tyr	Gly	Leu	Lys	Pro	Tyr	Ser	Pro

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	305	Leu	Ala	Ser	Leu	Ser	Gly	Glu	Pro	Pro	Gly	Arg	Phe	Gly	Glu	Pro	Asp	320
					325						330					335		
5		Arg	Val	Gly	Pro	Gln	Lys	Phe	Leu	Ser	Ala	Ala	Lys	Pro	Ala	Gly	Ala	
					340					345					350			
		Ser	Gly	Leu	Ser	Pro	Arg	Ile	Glu	Ile	Thr	Pro	Ser	His	Glu	Leu	Ile	
					355				360					365				
		Gln	Ala	Val	Gly	Pro	Leu	Arg	Met	Arg	Asp	Ala	Gly	Leu	Leu	Val	Glu	
					370				375					380				
10		Gln	Pro	Pro	Leu	Ala	Gly	Val	Ala	Ala	Ser	Pro	Arg	Phe	Thr	Leu	Pro	
							390					395					400	
		Val	Pro	Gly	Phe	Glu	Gly	Tyr	Arg	Glu	Pro	Leu	Cys	Leu	Ser	Pro	Ala	
						405					410					415		
		Ser	Ser	Gly	Ser	Ser	Ala	Ser	Phe	Ile	Ser	Asp	Thr	Phe	Ser	Pro	Tyr	
15					420					425					430			
		Thr	Ser	Pro	Cys	Val	Ser	Pro	Asn	Asn	Gly	Gly	Pro	Asp	Asp	Leu	Cys	
					435				440					445				
		Pro	Gln	Phe	Gln	Asn	Ile	Pro	Ala	His	Tyr	Ser	Pro	Arg	Thr	Ser	Pro	
					450				455				460					
20		Ile	Met	Ser	Pro	Arg	Thr	Ser	Leu	Ala	Glu	Asp	Ser	Cys	Leu	Gly	Arg	
							470					475					480	
		His	Ser	Pro	Val	Pro	Arg	Pro	Ala	Ser	Arg	Ser	Ser	Ser	Pro	Gly	Ala	
						485					490					495		
		Lys	Arg	Arg	His	Ser	Cys	Ala	Glu	Ala	Leu	Val	Ala	Leu	Pro	Pro	Gly	
25					500					505					510			
		Ala	Ser	Pro	Gln	Arg	Ser	Arg	Ser	Pro	Ser	Pro	Gln	Pro	Ser	Ser	His	
					515				520					525				
		Val	Ala	Pro	Gln	Asp	His	Gly	Ser	Pro	Ala	Gly	Tyr	Pro	Pro	Val	Ala	
					530				535				540					
30		Gly	Ser	Ala	Val	Ile	Met	Asp	Ala	Leu	Asn	Ser	Leu	Ala	Thr	Asp	Ser	
							550					555					560	
		Pro	Cys	Gly	Ile	Pro	Pro	Lys	Met	Trp	Lys	Thr	Ser	Pro	Asp	Pro	Ser	
						565					570					575		
		Pro	Val	Ser	Ala	Ala	Pro	Ser	Lys	Ala	Gly	Leu	Pro	Arg	His	Ile	Tyr	
35					580					585					590			
		Pro	Ala	Val	Glu	Phe	Leu	Gly	Pro	Cys	Glu	Gln	Gly	Glu	Arg	Arg	Asn	
					595				600					605				
		Ser	Ala	Pro	Glu	Ser	Ile	Leu	Leu	Val	Pro	Pro	Thr	Trp	Pro	Lys	Pro	
					610				615				620					
40		Leu	Val	Pro	Ala													

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	755		760		765
	Asn Ala Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys				
	770		775		780
5	Asn Thr Arg Val Arg Leu Val Phe Arg Val His Ile Pro Glu Ser Ser				
	785		790		795
	Gly Arg Ile Val Ser Leu Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser				800
		805		810	815
	Gln Arg Ser Ala His Glu Leu Pro Met Val Glu Arg Gln Asp Thr Asp				
		820		825	830
10	Ser Cys Leu Val Tyr Gly Gly Gln Gln Met Ile Leu Thr Gly Gln Asn				
		835		840	845
	Phe Thr Ser Glu Ser Lys Val Val Phe Thr Glu Lys Thr Thr Asp Gly				
		850		855	860
15	Gln Gln Ile Trp Glu Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln				
	865		870		875
	Pro Asn Met Leu Phe Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile				880
		885		890	895
	Arg Thr Pro Val Lys Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys				
		900		905	910
20	Arg Ser Gln Pro Gln His Phe Thr Tyr His Pro Val Pro Ala Ile Lys				
		915		920	925
	Thr Glu Pro Thr Asp Glu Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr				
		930		935	940
25	His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val				
	945		950		955
	Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln				
		965		970	975
	Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Gln Asn				
		980		985	990
30	Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu				
		995		1000	1005
	Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu Ala				
		1010		1015	1020
35	Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly Gln Ser				
	025		1030		1035
	Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala Ser Pro Val				1040
		1045		1050	1055
	Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys Gly Ser His Gln				
		1060		1065	1070
40	Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr				
		1075		1080	1085
	Arg Pro Gly Pro Pro Pro Val Ser Gln Gly Gln Arg Leu Ser Pro Gly				
		1090		1095	1100
45	Ser Tyr Pro Thr Val Ile Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala				
	105		1110		1115
	Ala Lys Asn Gly Pro Pro Val Ser Asp Gln Lys Glu Val Leu Pro Ala				1120
		1125		1130	1135
	Gly Val Thr Ile Lys Gln Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp				
		1140		1145	1150
50	Asp Val Asn Glu Ile Ile Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg				
		1155		1160	1165
	Asn Gln Thr				
	1170				

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(2) INFORMATION FOR SEQ ID NO:132:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...3543

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

15	ATG AAC GCC CCC GAG CGG CAG CCC CAA CCC GAC GGC GGG GAC GCC CCA	48
	Met Asn Ala Pro Glu Arg Gln Pro Gln Pro Asp Gly Gly Asp Ala Pro	
	1 5 10 15	
20	GGC CAC GAG CCT GGG GGC AGC CCC CAA GAC GAG CTT GAC TTC TCC ATC	96
	Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile	
	20 25 30	
25	CTC TTC GAC TAT GAG TAT TTG AAT CCG AAC GAA GAA GAG CCG AAT GCA	144
	Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala	
	35 40 45	
30	CAT AAG GTC GCC AGC CCA CCC TCC GGA CCC GCA TAC CCC GAT GAT GTA	192
	His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val	
	50 55 60	
35	ATG GAC TAT GGC CTC AAG CCA TAC AGC CCC CTT GCT AGT CTC TCT GGC	240
	Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly	
	65 70 75 80	
40	GAG CCC CCC GGC CGA TTC GGA GAG CCG GAT AGG GTA GGG CCG CAG AAG	288
	Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys	
	85 90 95	
45	TTT CTG AGC GCG GCC AAG CCA GCA GGG GCC TCG GGC CTG AGC CCT CGG	336
	Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala Ser Gly Leu Ser Pro Arg	
	100 105 110	
50	ATC GAG ATC ACT CCG TCC CAC GAA CTG ATC CAG GCA GTG GGG CCC CTC	384
	Ile Glu Ile Thr Pro Ser His Glu Leu Ile Gln Ala Val Gly Pro Leu	
	115 120 125	
55	CGC ATG AGA GAC GCG GGC CTC CTG GTG GAG CAG CCT CCC CTG GCC GGG	432
	Arg Met Arg Asp Ala Gly Leu Leu Val Glu Gln Pro Pro Leu Ala Gly	
	130 135 140	
60	GTG GCC GCC AGC CCG AGG TTC ACC CTG CCC GTG CCC GGC TTC GAG GGC	480
	Val Ala Ala Ser Pro Arg Phe Thr Leu Pro Val Pro Gly Phe Glu Gly	
	145 150 155 160	
65	TAC CGC GAG CCG CTT TGC TTG AGC CCC GCT AGC AGC GGC TCC TCT GCC	528

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	Tyr	Arg	Glu	Pro	Leu	Cys	Leu	Ser	Pro	Ala	Ser	Ser	Gly	Ser	Ser	Ala	
					165					170						175	
5	AGC	TTC	ATT	TCT	GAC	ACC	TTC	TCC	CCC	TAC	ACC	TCG	CCC	TGC	GTC	TCG	576
	Ser	Phe	Ile	Ser	Asp	Thr	Phe	Ser	Pro	Tyr	Thr	Ser	Pro	Cys	Val	Ser	
				180					185					190			
10	CCC	AAT	AAC	GGC	GGG	CCC	GAC	GAC	CTG	TGT	CCG	CAG	TTT	CAA	AAC	ATC	624
	Pro	Asn	Asn	Gly	Gly	Pro	Asp	Asp	Leu	Cys	Pro	Gln	Phe	Gln	Asn	Ile	
			195					200					205				
15	CCT	GCT	CAT	TAT	TCC	CCC	AGA	ACC	TCG	CCA	ATA	ATG	TCA	CCT	CGA	ACC	672
	Pro	Ala	His	Tyr	Ser	Pro	Arg	Thr	Ser	Pro	Ile	Met	Ser	Pro	Arg	Thr	
		210					215					220					
	AGC	CTC	GCC	GAG	GAC	AGC	TGC	CTG	GGC	CGC	CAC	TCG	CCC	GTG	CCC	CGT	720
	Ser	Leu	Ala	Glu	Asp	Ser	Cys	Leu	Gly	Arg	His	Ser	Pro	Val	Pro	Arg	
	225				230					235						240	
20	CCG	GCC	TCC	CGC	TCC	TCA	TCG	CCT	GGT	GCC	AAG	CGG	AGG	CAT	TCG	TGC	768
	Pro	Ala	Ser	Arg	Ser	Ser	Ser	Pro	Gly	Ala	Lys	Arg	Arg	His	Ser	Cys	
					245					250					255		
25	GCC	GAG	GCC	TTG	GTT	GCC	CTG	CCG	CCC	GGA	GCC	TCA	CCC	CAG	CGC	TCC	816
	Ala	Glu	Ala	Leu	Val	Ala	Leu	Pro	Pro	Gly	Ala	Ser	Pro	Gln	Arg	Ser	
				260					265					270			
30	CGG	AGC	CCC	TCG	CCG	CAG	CCC	TCA	TCT	CAC	GTG	GCA	CCC	CAG	GAC	CAC	864
	Arg	Ser	Pro	Ser	Pro	Gln	Pro	Ser	Ser	His	Val	Ala	Pro	Gln	Asp	His	
			275					280						285			
35	GGC	TCC	CCG	GCT	GGG	TAC	CCC	CCT	GTG	GCT	GGC	TCT	GCC	GTG	ATC	ATG	912
	Gly	Ser	Pro	Ala	Gly	Tyr	Pro	Pro	Val	Ala	Gly	Ser	Ala	Val	Ile	Met	
		290					295					300					
	GAT	GCC	CTG	AAC	AGC	CTC	GCC	ACG	GAC	TCG	CCT	TGT	GGG	ATC	CCC	CCC	960
	Asp	Ala	Leu	Asn	Ser	Leu	Ala	Thr	Asp	Ser	Pro	Cys	Gly	Ile	Pro	Pro	
	305					310					315				320		
40	AAG	ATG	TGG	AAG	ACC	AGC	CCT	GAC	CCC	TCG	CCG	GTG	TCT	GCC	GCC	CCA	1008
	Lys	Met	Trp	Lys	Thr	Ser	Pro	Asp	Pro	Ser	Pro	Val	Ser	Ala	Ala	Pro	
					325					330					335		
45	TCC	AAG	GCC	GGC	CTG	CCT	CGC	CAC	ATC	TAC	CCG	GCC	GTG	GAG	TTC	CTG	1056
	Ser	Lys	Ala	Gly	Leu	Pro	Arg	His	Ile	Tyr	Pro	Ala	Val	Glu	Phe	Leu	
				340					345					350			
50	GGG	CCC	TGC	GAG	CAG	GGC	GAG	AGG	AGA	AAC	TCG	GCT	CCA	GAA	TCC	ATC	1104
	Gly	Pro	Cys	Glu	Gln	Gly	Glu	Arg	Arg	Asn	Ser	Ala	Pro	Glu	Ser	Ile	
			355					360					365				
55	CTG	CTG	GTT	CCG	CCC	ACT	TGG	CCC	AAG	CCG	CTG	GTG	CCT	GCC	ATT	CCC	1152
	Leu	Leu	Val	Pro	Pro	Thr	Trp	Pro	Lys	Pro	Leu	Val	Pro	Ala	Ile	Pro	
		370					375					380					
	ATC	TGC	AGC	ATC	CCA	GTG	ACT	GCA	TCC	CTC	CCT	CCA	CTT	GAG	TGG	CCG	1200

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	Ile	Cys	Ser	Ile	Pro	Val	Thr	Ala	Ser	Leu	Pro	Pro	Leu	Glu	Trp	Pro	
	385					390				395						400	
5	CTG	TCC	AGT	CAG	TCA	GGC	TCT	TAC	GAG	CTG	CGG	ATC	GAG	GTG	CAG	CCC	1248
	Leu	Ser	Ser	Gln	Ser	Gly	Ser	Tyr	Glu	Leu	Arg	Ile	Glu	Val	Gln	Pro	
				405					410					415			
10	AAG	CCA	CAT	CAC	CGG	GCC	CAC	TAT	GAG	ACA	GAA	GGC	AGC	CGA	GGG	GCT	1296
	Lys	Pro	His	His	Arg	Ala	His	Tyr	Glu	Thr	Glu	Gly	Ser	Arg	Gly	Ala	
				420					425					430			
15	GTC	AAA	GCT	CCA	ACT	GGA	GGC	CAC	CCT	GTG	GTT	CAG	CTC	CAT	GGC	TAC	1344
	Val	Lys	Ala	Pro	Thr	Gly	Gly	His	Pro	Val	Val	Gln	Leu	His	Gly	Tyr	
			435					440						445			
20	ATG	GAA	AAC	AAG	CCT	CTG	GGA	CTT	CAG	ATC	TTC	ATT	GGG	ACA	GCT	GAT	1392
	Met	Glu	Asn	Lys	Pro	Leu	Gly	Leu	Gln	Ile	Phe	Ile	Gly	Thr	Ala	Asp	
		450					455					460					
25	GAG	CGG	ATC	CTT	AAG	CCG	CAC	GCC	TTC	TAC	CAG	GTG	CAC	CGA	ATC	ACG	1440
	Glu	Arg	Ile	Leu	Lys	Pro	His	Ala	Phe	Tyr	Gln	Val	His	Arg	Ile	Thr	
	465					470					475					480	
30	GGG	AAA	ACT	GTC	ACC	ACC	ACC	AGC	TAT	GAG	AAG	ATA	GTG	GGC	AAC	ACC	1488
	Gly	Lys	Thr	Val	Thr	Thr	Thr	Ser	Tyr	Glu	Lys	Ile	Val	Gly	Asn	Thr	
				485						490					495		
35	AAA	GTC	CTG	GAG	ATC	CCC	TTG	GAG	CCC	AAA	AAC	AAC	ATG	AGG	GCA	ACC	1536
	Lys	Val	Leu	Glu	Ile	Pro	Leu	Glu	Pro	Lys	Asn	Asn	Met	Arg	Ala	Thr	
				500					505					510			
40	ATC	GAC	TGT	GCG	GGG	ATC	TTG	AAG	CTT	AGA	AAC	GCC	GAC	ATT	GAG	CTG	1584
	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Lys	Leu	Arg	Asn	Ala	Asp	Ile	Glu	Leu	
			515					520					525				
45	CGG	AAA	GGC	GAG	ACG	GAC	ATT	GGA	AGA	AAG	AAC	ACG	CGG	GTG	AGA	CTG	1632
	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	Arg	Lys	Asn	Thr	Arg	Val	Arg	Leu	
		530						535					540				
50	GTT	TTC	CGA	GTT	CAC	ATC	CCA	GAG	TCC	AGT	GGC	AGA	ATC	GTC	TCT	TTA	1680
	Val	Phe	Arg	Val	His	Ile	Pro	Glu	Ser	Ser	Gly	Arg	Ile	Val	Ser	Leu	
	545					550					555					560	
55	CAG	ACT	GCA	TCT	AAC	CCC	ATC	GAG	TGC	TCC	CAG	CGA	TCT	GCT	CAC	GAG	1728
	Gln	Thr	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	Gln	Arg	Ser	Ala	His	Glu	
				565					570					575			
60	CTG	CCC	ATG	GTT	GAA	AGA	CAA	GAC	ACA	GAC	AGC	TGC	CTG	GTC	TAT	GGC	1776
	Leu	Pro	Met	Val	Glu	Arg	Gln	Asp	Thr	Asp	Ser	Cys	Leu	Val	Tyr	Gly	
				580					585					590			
65	GGC	CAG	CAA	ATG	ATC	CTC	ACG	GGG	CAG	AAC	TTT	ACA	TCC	GAG	TCC	AAA	1824
	Gly	Gln	Gln	Met	Ile	Leu	Thr	Gly	Gln	Asn	Phe	Thr	Ser	Glu	Ser	Lys	
			595					600						605			
70	GTT	GTG	TTT	ACT	GAG	AAG	ACC	ACA	GAT	GGA	CAG	CAA	ATT	TGG	GAG	ATG	1872

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	Val	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly	Gln	Gln	Ile	Trp	Glu	Met	
	610						615				620						
5	GAA	GCC	ACG	GTG	GAT	AAG	GAC	AAG	AGC	CAG	CCC	AAC	ATG	CTT	TTT	GTT	1920
	Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	Pro	Asn	Met	Leu	Phe	Val	
	625					630				635						640	
10	GAG	ATC	CCT	GAA	TAT	CGG	AAC	AAG	CAT	ATC	CGC	ACA	CCT	GTA	AAA	GTG	1968
	Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	Arg	Thr	Pro	Val	Lys	Val	
					645					650					655		
15	AAC	TTC	TAC	GTC	ATC	AAT	GGG	AAG	AGA	AAA	CGA	AGT	CAG	CCT	CAG	CAC	2016
	Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Pro	Gln	His	
				660					665					670			
20	TTT	ACC	TAC	CAC	CCA	GTC	CCA	GCC	ATC	AAG	ACG	GAG	CCC	ACG	GAT	GAA	2064
	Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	Thr	Glu	Pro	Thr	Asp	Glu	
				675				680					685				
25	TAT	GAC	CCC	ACT	CTG	ATC	TGC	AGC	CCC	ACC	CAT	GGA	GGC	CTG	GGG	AGC	2112
	Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	His	Gly	Gly	Leu	Gly	Ser	
		690					695					700					
30	CAG	CCT	TAC	TAC	CCC	CAG	CAC	CCG	ATG	GTG	GCC	GAG	TCC	CCC	TCC	TGC	2160
	Gln	Pro	Tyr	Tyr	Pro	Gln	His	Pro	Met	Val	Ala	Glu	Ser	Pro	Ser	Cys	
	705					710				715						720	
35	CTC	GTG	GCC	ACC	ATG	GCT	CCC	TGC	CAG	CAG	TTC	CGC	ACG	GGG	CTC	TCA	2208
	Leu	Val	Ala	Thr	Met	Ala	Pro	Cys	Gln	Gln	Phe	Arg	Thr	Gly	Leu	Ser	
					725				730						735		
40	TCC	CCT	GAC	GCC	CGC	TAC	CAG	CAA	CAG	AAC	CCA	GCG	GCC	GTA	CTC	TAC	2256
	Ser	Pro	Asp	Ala	Arg	Tyr	Gln	Gln	Gln	Asn	Pro	Ala	Ala	Val	Leu	Tyr	
				740					745					750			
45	CAG	CGG	AGC	AAG	AGC	CTG	AGC	CCC	AGC	CTG	CTG	GGC	TAT	CAG	CAG	CCG	2304
	Gln	Arg	Ser	Lys	Ser	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Tyr	Gln	Gln	Pro	
			755					760					765				
50	GCC	CTC	ATG	GCC	GCC	CCG	CTG	TCC	CTT	GCG	GAC	GCT	CAC	CGC	TCT	GTG	2352
	Ala	Leu	Met	Ala	Ala	Pro	Leu	Ser	Leu	Ala	Asp	Ala	His	Arg	Ser	Val	
		770					775					780					
55	CTG	GTG	CAC	GCC	GGC	TCC	CAG	GGC	CAG	AGC	TCA	GCC	CTG	CTC	CAC	CCC	2400
	Leu	Val	His	Ala	Gly	Ser	Gln	Gly	Gln	Ser	Ser	Ala	Leu	Leu	His	Pro	
	785					790					795					800	
60	TCT	CCG	ACC	AAC	CAG	CAG	GCC	TCG	CCT	GTG	ATC	CAC	TAC	TCA	CCC	ACC	2448
	Ser	Pro	Thr	Asn	Gln	Gln	Ala	Ser	Pro	Val	Ile	His	Tyr	Ser	Pro	Thr	
					805					810					815		
65	AAC	CAG	CAG	CTG	CGC	TGC	GGA	AGC	CAC	CAG	GAG	TTC	CAG	CAC	ATC	ATG	2496
	Asn	Gln	Gln	Leu	Arg	Cys	Gly	Ser	His	Gln	Glu	Phe	Gln	His	Ile	Met	
				820					825					830			
70	TAC	TGC	GAG	AAT	TTC	GCA	CCA	GGC	ACC	ACC	AGA	CCT	GGC	CCG	CCC	CCG	2544

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	Tyr	Cys	Glu	Asn	Phe	Ala	Pro	Gly	Thr	Thr	Arg	Pro	Gly	Pro	Pro	Pro	
			835					840					845				
5	GTC	AGT	CAA	GGT	CAG	AGG	CTG	AGC	CCG	GGT	TCC	TAC	CCC	ACA	GTC	ATT	2592
	Val	Ser	Gln	Gly	Gln	Arg	Leu	Ser	Pro	Gly	Ser	Tyr	Pro	Thr	Val	Ile	
		850					855					860					
10	CAG	CAG	CAG	AAT	GCC	ACG	AGC	CAA	AGA	GCC	GCC	AAA	AAC	GGA	CCC	CCG	2640
	Gln	Gln	Gln	Asn	Ala	Thr	Ser	Gln	Arg	Ala	Ala	Lys	Asn	Gly	Pro	Pro	
	865					870				875						880	
15	GTC	AGT	GAC	CAA	AAG	GAA	GTA	TTA	CCT	GCG	GGG	GTG	ACC	ATT	AAA	CAG	2688
	Val	Ser	Asp	Gln	Lys	Glu	Val	Leu	Pro	Ala	Gly	Val	Thr	Ile	Lys	Gln	
					885					890					895		
20	GAG	CAG	AAC	TTG	GAC	CAG	ACC	TAC	TTG	GAT	GAT	GTT	AAT	GAA	ATT	ATC	2736
	Glu	Gln	Asn	Leu	Asp	Gln	Thr	Tyr	Leu	Asp	Asp	Val	Asn	Glu	Ile	Ile	
				900					905					910			
25	AGG	AAG	GAG	TTT	TCA	GGA	CCT	CCT	GCC	AGA	AAT	CAG	ACG	AGA	ATT	CTG	2784
	Arg	Lys	Glu	Phe	Ser	Gly	Pro	Pro	Ala	Arg	Asn	Gln	Thr	Arg	Ile	Leu	
			915				920					925					
30	CAG	TCG	ACG	GTA	CCG	CGG	GCC	CGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	2832
	Gln	Ser	Thr	Val	Pro	Arg	Ala	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	
		930				935						940					
35	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	2880
	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
	945					950				955						960	
40	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	2928
	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
					965				970						975		
45	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	2976
	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	
				980				985						990			
50	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	3024
	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	
			995				1000					1005					
55	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	3072
	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	
		1010					1015				1020						
60	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTG	CAG	GAG	CGC	ACC	3120
	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	
	1025				1030					1035					1040		
65	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	3168
	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	
					1045			1050						1055			
70	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	3216

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Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 1060 1065 1070

5 TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC 3264
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 1075 1080 1085

10 AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC 3312
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 1090 1095 1100

15 AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG 3360
 Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
 1105 1110 1115 1120

CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG 3408
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 1125 1130 1135

20 CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA 3456
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
 1140 1145 1150

25 GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC 3504
 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 1155 1160 1165

30 GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 3546
 Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:133:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1181 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Asn Ala Pro Glu Arg Gln Pro Gln Pro Asp Gly Gly Asp Ala Pro
 1 5 10 15
 Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile
 20 25 30
 50 Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala
 35 40 45
 His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val
 50 55 60
 Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly
 55 65 70 75 80
 Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys

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				85				90				95				
	Phe	Leu	Ser	Ala	Ala	Lys	Pro	Ala	Gly	Ala	Ser	Gly	Leu	Ser	Pro	Arg
				100					105				110			
5	Ile	Glu	Ile	Thr	Pro	Ser	His	Glu	Leu	Ile	Gln	Ala	Val	Gly	Pro	Leu
			115					120					125			
	Arg	Met	Arg	Asp	Ala	Gly	Leu	Leu	Val	Glu	Gln	Pro	Pro	Leu	Ala	Gly
		130				135					140					
	Val	Ala	Ala	Ser	Pro	Arg	Phe	Thr	Leu	Pro	Val	Pro	Gly	Phe	Glu	Gly
	145					150				155					160	
10	Tyr	Arg	Glu	Pro	Leu	Cys	Leu	Ser	Pro	Ala	Ser	Ser	Gly	Ser	Ser	Ala
				165					170					175		
	Ser	Phe	Ile	Ser	Asp	Thr	Phe	Ser	Pro	Tyr	Thr	Ser	Pro	Cys	Val	Ser
			180						185				190			
15	Pro	Asn	Asn	Gly	Gly	Pro	Asp	Asp	Leu	Cys	Pro	Gln	Phe	Gln	Asn	Ile
		195					200					205				
	Pro	Ala	His	Tyr	Ser	Pro	Arg	Thr	Ser	Pro	Ile	Met	Ser	Pro	Arg	Thr
	210					215				220						
	Ser	Leu	Ala	Glu	Asp	Ser	Cys	Leu	Gly	Arg	His	Ser	Pro	Val	Pro	Arg
	225				230					235					240	
20	Pro	Ala	Ser	Arg	Ser	Ser	Ser	Pro	Gly	Ala	Lys	Arg	Arg	His	Ser	Cys
				245					250					255		
	Ala	Glu	Ala	Leu	Val	Ala	Leu	Pro	Pro	Gly	Ala	Ser	Pro	Gln	Arg	Ser
		260						265					270			
25	Arg	Ser	Pro	Ser	Pro	Gln	Pro	Ser	Ser	His	Val	Ala	Pro	Gln	Asp	His
		275					280					285				
	Gly	Ser	Pro	Ala	Gly	Tyr	Pro	Pro	Val	Ala	Gly	Ser	Ala	Val	Ile	Met
	290					295				300						
	Asp	Ala	Leu	Asn	Ser	Leu	Ala	Thr	Asp	Ser	Pro	Cys	Gly	Ile	Pro	Pro
	305			310					315					320		
30	Lys	Met	Trp	Lys	Thr	Ser	Pro	Asp	Pro	Ser	Pro	Val	Ser	Ala	Ala	Pro
				325					330					335		
	Ser	Lys	Ala	Gly	Leu	Pro	Arg	His	Ile	Tyr	Pro	Ala	Val	Glu	Phe	Leu
			340					345				350				
35	Gly	Pro	Cys	Glu	Gln	Gly	Glu	Arg	Arg	Asn	Ser	Ala	Pro	Glu	Ser	Ile
		355				360				365						
	Leu	Leu	Val	Pro	Pro	Thr	Trp	Pro	Lys	Pro	Leu	Val	Pro	Ala	Ile	Pro
	370					375				380						
	Ile	Cys	Ser	Ile	Pro	Val	Thr	Ala	Ser	Leu	Pro	Pro	Leu	Glu	Trp	Pro
	385			390				395					400			
40	Leu	Ser	Ser	Gln	Ser	Gly	Ser	Tyr	Glu	Leu	Arg	Ile	Glu	Val	Gln	Pro
				405				410					415			
	Lys	Pro	His	His	Arg	Ala	His	Tyr	Glu	Thr	Glu	Gly	Ser	Arg	Gly	Ala
			420					425				430				
45	Val	Lys	Ala	Pro	Thr	Gly	Gly	His	Pro	Val	Val	Gln	Leu	His	Gly	Tyr
		435				440				445						
	Met	Glu	Asn	Lys	Pro	Leu	Gly	Leu	Gln	Ile	Phe	Ile	Gly	Thr	Ala	Asp
	450					455				460						
	Glu	Arg	Ile	Leu	Lys	Pro	His	Ala	Phe	Tyr	Gln	Val	His	Arg	Ile	Thr
	465			470				475					480			
50	Gly	Lys	Thr	Val	Thr	Thr	Ser	Tyr	Glu	Lys	Ile	Val	Gly	Asn	Thr	
				485				490					495			
	Lys	Val	Leu	Glu	Ile	Pro	Leu	Glu	Pro	Lys	Asn	Asn	Met	Arg	Ala	Thr
		500						505				510				
55	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Lys	Leu	Arg	Asn	Ala	Asp	Ile	Glu	Leu
		515				520						525				
	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	Arg	Lys	Asn	Thr	Arg	Val	Arg	Leu

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		530				535					540					
	Val	Phe	Arg	Val	His	Ile	Pro	Glu	Ser	Ser	Gly	Arg	Ile	Val	Ser	Leu
	545					550					555					560
	Gln	Thr	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	Gln	Arg	Ser	Ala	His	Glu
5					565					570					575	
	Leu	Pro	Met	Val	Glu	Arg	Gln	Asp	Thr	Asp	Ser	Cys	Leu	Val	Tyr	Gly
				580				585						590		
	Gly	Gln	Gln	Met	Ile	Leu	Thr	Gly	Gln	Asn	Phe	Thr	Ser	Glu	Ser	Lys
			595					600					605			
10	Val	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly	Gln	Gln	Ile	Trp	Glu	Met
	610						615					620				
	Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	Pro	Asn	Met	Leu	Phe	Val
	625				630					635						640
	Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	Arg	Thr	Pro	Val	Lys	Val
15					645				650						655	
	Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Pro	Gln	His
				660				665						670		
	Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	Thr	Glu	Pro	Thr	Asp	Glu
			675				680						685			
20	Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	His	Gly	Gly	Leu	Gly	Ser
	690						695					700				
	Gln	Pro	Tyr	Tyr	Pro	Gln	His	Pro	Met	Val	Ala	Glu	Ser	Pro	Ser	Cys
	705				710					715						720
	Leu	Val	Ala	Thr	Met	Ala	Pro	Cys	Gln	Gln	Phe	Arg	Thr	Gly	Leu	Ser
25					725					730					735	
	Ser	Pro	Asp	Ala	Arg	Tyr	Gln	Gln	Gln	Asn	Pro	Ala	Ala	Val	Leu	Tyr
				740				745					750			
	Gln	Arg	Ser	Lys	Ser	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Tyr	Gln	Gln	Pro
			755				760					765				
30	Ala	Leu	Met	Ala	Ala	Pro	Leu	Ser	Leu	Ala	Asp	Ala	His	Arg	Ser	Val
	770						775					780				
	Leu	Val	His	Ala	Gly	Ser	Gln	Gly	Gln	Ser	Ser	Ala	Leu	Leu	His	Pro
	785				790					795						800
	Ser	Pro	Thr	Asn	Gln	Gln	Ala	Ser	Pro	Val	Ile	His	Tyr	Ser	Pro	Thr
35				805						810					815	
	Asn	Gln	Gln	Leu	Arg	Cys	Gly	Ser	His	Gln	Glu	Phe	Gln	His	Ile	Met
				820				825					830			
	Tyr	Cys	Glu	Asn	Phe	Ala	Pro	Gly	Thr	Thr	Arg	Pro	Gly	Pro	Pro	Pro
			835				840						845			
40	Val	Ser	Gln	Gly	Gln	Arg	Leu	Ser	Pro	Gly	Ser	Tyr	Pro	Thr	Val	Ile
	850						855					860				
	Gln	Gln	Gln	Asn	Ala	Thr	Ser	Gln	Arg	Ala	Ala	Lys	Asn	Gly	Pro	Pro

SUBSTITUTE SHEET (RULE 26)

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	980	985	990
	Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr		
	995	1000	1005
5	Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His		
	1010	1015	1020
	Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr		
	025	1030	1035
	Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys		
	1045	1050	1055
10	Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp		
	1060	1065	1070
	Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr		
	1075	1080	1085
15	Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile		
	1090	1095	1100
	Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln		
	105	1110	1115
	Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val		
	1125	1130	1135
20	Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys		
	1140	1145	1150
	Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr		
	1155	1160	1165
25	Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
	1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 2802 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...2799
 40 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

45	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
50	20 25 30	
	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
55	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192

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	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50						55					60					
5	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75						80	
10	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
15	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
20	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
25	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
30	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
35	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
40	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
45	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
50	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
55	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
60	GGA	CTC	AGA	TCT	CGA	GGG	AGC	ATG	GGC	ACC	TTG	CGG	GAT	TTA	CAG	TAC	768
	Gly	Leu	Arg	Ser	Arg	Gly	Ser	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	
					245					250					255		
65	GCG	CTC	CAG	GAG	AAG	ATC	GAG	GAG	CTG	AGG	CAG	CGG	GAT	GCT	CTC	ATC	816
	Ala	Leu	Gln	Glu	Lys	Ile	Glu	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	
				260					265					270			
70	GAC	GAG	CTG	GAG	CTG	GAG	TTG	GAT	CAG	AAG	GAC	GAA	CTG	ATC	CAG	AAG	864

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	Asp	Glu	Leu	Glu	Leu	Glu	Leu	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys		
	275							280						285				
5	CTG	CAG	AAC	GAG	CTG	GAC	AAG	TAC	CGC	TCG	GTG	ATC	CGA	CCA	GCC	ACC	912	
	Leu	Gln	Asn	Glu	Leu	Asp	Lys	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr		
	290						295					300						
10	CAG	CAG	GCG	CAG	AAG	CAG	AGC	GCG	AGC	ACC	TTG	CAG	GGC	GAG	CCG	CGC	960	
	Gln	Gln	Ala	Gln	Lys	Gln	Ser	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg		
	305					310					315				320			
15	ACC	AAG	CGG	CAG	GCG	ATC	TCC	GCC	GAG	CCC	ACC	GCC	TTC	GAC	ATC	CAG	1008	
	Thr	Lys	Arg	Gln	Ala	Ile	Ser	Ala	Glu	Pro	Thr	Ala	Phe	Asp	Ile	Gln		
				325						330						335		
20	GAT	CTC	AGC	CAT	GTG	ACC	CTG	CCC	TTC	TAC	CCC	AAG	AGC	CCA	CAG	TCC	1056	
	Asp	Leu	Ser	His	Val	Thr	Leu	Pro	Phe	Tyr	Pro	Lys	Ser	Pro	Gln	Ser		
				340						345						350		
25	AAG	GAT	CTT	ATA	AAG	GAA	GCT	ATC	CTT	GAC	AAT	GAC	TTT	ATG	AAG	AAC	1104	
	Lys	Asp	Leu	Ile	Lys	Glu	Ala	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn		
	355						360						365					
30	TTG	GAG	CTG	TCG	CAG	ATC	CAG	GAG	ATT	GTG	GAT	TGT	ATG	TAC	CCG	GTG	1152	
	Leu	Glu	Leu	Ser	Gln	Ile	Gln	Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val		
	370						375						380					
35	GAG	TAT	GGC	AAG	GAC	AGT	TGC	ATC	ATC	AAA	GAA	GGA	GAC	GTG	GGG	TCA	1200	
	Glu	Tyr	Gly	Lys	Asp	Ser	Cys	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser		
	385			390						395						400		
40	CTG	GTG	TAT	GTC	ATG	GAA	GAT	GGT	AAG	GTT	GAA	GTT	ACA	AAA	GAA	GGT	1248	
	Leu	Val	Tyr	Val	Met	Glu	Asp	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly		
				405						410						415		
45	GTG	AAG	TTG	TGT	ACC	ATG	GGT	CCA	GGA	AAA	GTG	TTT	GGG	GAA	TTG	GCT	1296	
	Val	Lys	Leu	Cys	Thr	Met	Gly	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala		
				420						425						430		
50	ATT	CTT	TAC	AAC	TGT	ACC	CGG	ACA	GCG	ACC	GTC	AAG	ACT	CTT	GTA	AAT	1344	
	Ile	Leu	Tyr	Asn	Cys	Thr	Arg	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn		
	435						440						445					
55	GTA	AAA	CTC	TGG	GCC	ATT	GAT	CGA	CAA	TGT	TTT	CAA	ACA	ATA	ATG	ATG	1392	
	Val	Lys	Leu	Trp	Ala	Ile	Asp	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met		
	450						455						460					
60	AGG	ACA	GGA	CTC	ATC	AAG	CAT	ACC	GAG	TAT	ATG	GAA	TTT	TTA	AAA	AGC	1440	
	Arg	Thr	Gly	Leu	Ile	Lys	His	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser		
	465			470						475						480		
65	GTT	CCA	ACA	TTC	CAG	AGC	CTT	CCT	GAA	GAG	ATC	CTC	AGC	AAG	CTT	GCT	1488	
	Val	Pro	Thr	Phe	Gln	Ser	Leu	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala		
				485						490						495		
70	GAT	GTC	CTT	GAA	GAG	ACC	CAC	TAT	GAA	AAT	GGA	GAA	TAT	ATT	ATC	AGG	1536	

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	Asp	Val	Leu	Glu	Glu	Thr	His	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	
				500					505					510			
5	CAA	GGT	GCA	AGA	GGG	GAC	ACC	TTC	TTT	ATC	ATC	AGC	AAA	GGA	ACG	GTA	1584
	Gln	Gly	Ala	Arg	Gly	Asp	Thr	Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val	
			515					520					525				
10	AAT	GTC	ACT	CGT	GAA	GAC	TCA	CCG	AGT	GAA	GAC	CCA	GTC	TTT	CTT	AGA	1632
	Asn	Val	Thr	Arg	Glu	Asp	Ser	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg	
			530				535					540					
15	ACT	TTA	GGA	AAA	GGA	GAC	TGG	TTT	GGA	GAG	AAA	GCC	TTG	CAG	GGG	GAA	1680
	Thr	Leu	Gly	Lys	Gly	Asp	Trp	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu	
	545					550					555					560	
	GAT	GTG	AGA	ACA	GCA	AAC	GTA	ATT	GCT	GCA	GAA	GCT	GTA	ACC	TGC	CTT	1728
	Asp	Val	Arg	Thr	Ala	Asn	Val	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu	
					565					570					575		
20	GTG	ATT	GAC	AGA	GAC	TCT	TTT	AAA	CAT	TTG	ATT	GGA	GGG	CTG	GAT	GAT	1776
	Val	Ile	Asp	Arg	Asp	Ser	Phe	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp	
				580					585					590			
25	GTT	TCT	AAT	AAA	GCA	TAT	GAA	GAT	GCA	GAA	GCT	AAA	GCA	AAA	TAT	GAA	1824
	Val	Ser	Asn	Lys	Ala	Tyr	Glu	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu	
			595					600					605				
30	GCT	GAA	GCG	GCT	TTC	TTC	GCC	AAC	CTG	AAG	CTG	TCT	GAT	TTC	AAC	ATC	1872
	Ala	Glu	Ala	Ala	Phe	Phe	Ala	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile	
		610					615						620				
35	ATT	GAT	ACC	CTT	GGA	GTT	GGA	GGT	TTC	GGA	CGA	GTA	GAA	CTG	GTC	CAG	1920
	Ile	Asp	Thr	Leu	Gly	Val	Gly	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln	
	625					630					635					640	
	TTG	AAA	AGT	GAA	GAA	TCC	AAA	ACG	TTT	GCA	ATG	AAG	ATT	CTC	AAG	AAA	1968
	Leu	Lys	Ser	Glu	Glu	Ser	Lys	Thr	Phe	Ala	Met	Lys	Ile	Leu	Lys	Lys	
					645					650					655		
40	CGT	CAC	ATT	GTG	GAC	ACA	AGA	CAG	CAG	GAG	CAC	ATC	CGC	TCA	GAG	AAG	2016
	Arg	His	Ile	Val	Asp	Thr	Arg	Gln	Gln	Glu	His	Ile	Arg	Ser	Glu	Lys	
				660					665					670			
45	CAG	ATC	ATG	CAG	GGG	GCT	CAT	TCC	GAT	TTC	ATA	GTG	AGA	CTG	TAC	AGA	2064
	Gln	Ile	Met	Gln	Gly	Ala	His	Ser	Asp	Phe	Ile	Val	Arg	Leu	Tyr	Arg	
			675						680					685			
50	ACA	TTT	AAG	GAC	AGC	AAA	TAT	TTG	TAT	ATG	TTG	ATG	GAA	GCT	TGT	CTA	2112
	Thr	Phe	Lys	Asp	Ser	Lys	Tyr	Leu	Tyr	Met	Leu	Met	Glu	Ala	Cys	Leu	
		690					695					700					
55	GGT	GGA	GAG	CTC	TGG	ACC	ATT	CTC	AGG	GAT	AGA	GGT	TCG	TTT	GAA	GAT	2160
	Gly	Gly	Glu	Leu	Trp	Thr	Ile	Leu	Arg	Asp	Arg	Gly	Ser	Phe	Glu	Asp	
	705					710					715					720	
	TCT	ACA	ACC	AGA	TTT	TAC	ACA	GCA	TGT	GTG	GTA	GAA	GCT	TTT	GCC	TAT	2208

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	Ser	Thr	Thr	Arg	Phe	Tyr	Thr	Ala	Cys	Val	Val	Glu	Ala	Phe	Ala	Tyr	
					725					730					735		
5	CTG	CAT	TCC	AAA	GGA	ATC	ATT	TAC	AGG	GAC	CTC	AAG	CCA	GAA	AAT	CTC	2256
	Leu	His	Ser	Lys	Gly	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	
				740					745					750			
10	ATC	CTA	GAT	CAC	CGA	GGT	TAT	GCC	AAA	CTG	GTT	GAT	TTT	GGC	TTT	GCA	2304
	Ile	Leu	Asp	His	Arg	Gly	Tyr	Ala	Lys	Leu	Val	Asp	Phe	Gly	Phe	Ala	
				755				760					765				
15	AAG	AAA	ATA	GGA	TTT	GGA	AAG	AAA	ACA	TGG	ACT	TTT	TGT	GGG	ACT	CCA	2352
	Lys	Lys	Ile	Gly	Phe	Gly	Lys	Lys	Thr	Trp	Thr	Phe	Cys	Gly	Thr	Pro	
				770				775				780					
20	GAG	TAT	GTA	GCC	CCA	GAG	ATC	ATC	CTG	AAC	AAA	GGC	CAT	GAC	ATT	TCA	2400
	Glu	Tyr	Val	Ala	Pro	Glu	Ile	Ile	Leu	Asn	Lys	Gly	His	Asp	Ile	Ser	
	785					790					795					800	
25	GCC	GAC	TAC	TGG	TCA	CTG	GGA	ATC	CTA	ATG	TAT	GAA	CTC	CTG	ACT	GGC	2448
	Ala	Asp	Tyr	Trp	Ser	Leu	Gly	Ile	Leu	Met	Tyr	Glu	Leu	Leu	Thr	Gly	
					805					810					815		
30	AGC	CCA	CCT	TTC	TCA	GGC	CCA	GAT	CCT	ATG	AAA	ACC	TAT	AAC	ATC	ATA	2496
	Ser	Pro	Pro	Phe	Ser	Gly	Pro	Asp	Pro	Met	Lys	Thr	Tyr	Asn	Ile	Ile	
				820					825					830			
35	TTG	AGG	GGG	ATT	GAC	ATG	ATA	GAA	TTT	CCA	AAG	AAG	ATT	GCC	AAA	AAT	2544
	Leu	Arg	Gly	Ile	Asp	Met	Ile	Glu	Phe	Pro	Lys	Lys	Ile	Ala	Lys	Asn	
				835				840					845				
40	GCT	GCT	AAT	TTA	ATT	AAA	AAA	CTA	TGC	AGG	GAC	AAT	CCA	TCA	GAA	AGA	2592
	Ala	Ala	Asn	Leu	Ile	Lys	Lys	Leu	Cys	Arg	Asp	Asn	Pro	Ser	Glu	Arg	
				850				855				860					
45	TTA	GGG	AAT	TTG	AAA	AAT	GGA	GTA	AAA	GAC	ATT	CAA	AAG	CAC	AAA	TGG	2640
	Leu	Gly	Asn	Leu	Lys	Asn	Gly	Val	Lys	Asp	Ile	Gln	Lys	His	Lys	Trp	
	865					870				875						880	
50	TTT	GAG	GGC	TTT	AAC	TGG	GAA	GGC	TTA	AGA	AAA	GGT	ACC	TTG	ACA	CCT	2688
	Phe	Glu	Gly	Phe	Asn	Trp	Glu	Gly	Leu	Arg	Lys	Gly	Thr	Leu	Thr	Pro	
					885				890					895			
55	CCT	ATA	ATA	CCA	AGT	GTT	GCA	TCA	CCC	ACA	GAC	ACA	AGT	AAT	TTT	GAC	2736
	Pro	Ile	Ile	Pro	Ser	Val	Ala	Ser	Pro	Thr	Asp	Thr	Ser	Asn	Phe	Asp	
				900					905					910			
60	AGT	TTC	CCT	GAG	GAC	AAC	GAT	GAA	CCA	CCA	CCT	GAT	GAC	AAC	TCA	GGA	2784
	Ser	Phe	Pro	Glu	Asp	Asn	Asp	Glu	Pro	Pro	Pro	Asp	Asp	Asn	Ser	Gly	
				915				920					925				
65	TGG	GAT	ATA	GAC	TTC	TAA											2802
	Trp	Asp	Ile	Asp	Phe												
				930													

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(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 933 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 10 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

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15 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
    1      5      10      15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
    20      25      30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
    35      40      45
20 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50      55      60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
    65      70      75      80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
25      85      90      95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
    100      105      110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
    115      120      125
30 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130      135      140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
    145      150      155      160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
35      165      170      175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
    180      185      190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
    195      200      205
40 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210      215      220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
    225      230      235      240
Gly Leu Arg Ser Arg Gly Ser Met Gly Thr Leu Arg Asp Leu Gln Tyr
45      245      250      255
Ala Leu Gln Glu Lys Ile Glu Glu Leu Arg Gln Arg Asp Ala Leu Ile
    260      265      270
Asp Glu Leu Glu Leu Glu Leu Asp Gln Lys Asp Glu Leu Ile Gln Lys
    275      280      285
50 Leu Gln Asn Glu Leu Asp Lys Tyr Arg Ser Val Ile Arg Pro Ala Thr
    290      295      300
Gln Gln Ala Gln Lys Gln Ser Ala Ser Thr Leu Gln Gly Glu Pro Arg
    305      310      315      320
Thr Lys Arg Gln Ala Ile Ser Ala Glu Pro Thr Ala Phe Asp Ile Gln
55      325      330      335
Asp Leu Ser His Val Thr Leu Pro Phe Tyr Pro Lys Ser Pro Gln Ser

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			340				345				350					
	Lys	Asp	Leu	Ile	Lys	Glu	Ala	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn
			355					360					365			
5	Leu	Glu	Leu	Ser	Gln	Ile	Gln	Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val
			370				375				380					
	Glu	Tyr	Gly	Lys	Asp	Ser	Cys	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser
	385				390				395					400		
	Leu	Val	Tyr	Val	Met	Glu	Asp	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly
				405				410					415			
10	Val	Lys	Leu	Cys	Thr	Met	Gly	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala
			420					425					430			
	Ile	Leu	Tyr	Asn	Cys	Thr	Arg	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn
			435					440					445			
15	Val	Lys	Leu	Trp	Ala	Ile	Asp	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met
		450					455				460					
	Arg	Thr	Gly	Leu	Ile	Lys	His	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser
	465				470				475					480		
	Val	Pro	Thr	Phe	Gln	Ser	Leu	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala
				485				490						495		
20	Asp	Val	Leu	Glu	Thr	His	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	
			500					505					510			
	Gln	Gly	Ala	Arg	Gly	Asp	Thr	Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val
			515					520					525			
25	Asn	Val	Thr	Arg	Glu	Asp	Ser	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg
		530				535					540					
	Thr	Leu	Gly	Lys	Gly	Asp	Trp	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu
	545				550				555				560			
	Asp	Val	Arg	Thr	Ala	Asn	Val	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu
				565				570					575			
30	Val	Ile	Asp	Arg	Asp	Ser	Phe	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp
			580					585					590			
	Val	Ser	Asn	Lys	Ala	Tyr	Glu	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu
			595				600					605				
35	Ala	Glu	Ala	Ala	Phe	Phe	Ala	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile
		610				615					620					
	Ile	Asp	Thr	Leu	Gly	Val	Gly	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln
	625				630				635				640			
	Leu	Lys	Ser	Glu	Glu	Ser	Lys	Thr	Phe	Ala	Met	Lys	Ile	Leu	Lys	Lys
				645				650					655			
40	Arg	His	Ile	Val	Asp	Thr	Arg	Gln	Gln	Glu	His	Ile	Arg	Ser	Glu	Lys
			660					665					670			
	Gln	Ile	Met	Gln	Gly	Ala	His	Ser	Asp	Phe	Ile	Val	Arg	Leu	Tyr	Arg
		675					680					685				
45	Thr	Phe	Lys	Asp	Ser	Lys	Tyr	Leu	Tyr	Met	Leu	Met	Glu	Ala	Cys	Leu
		690				695					700					
	Gly	Gly	Glu	Leu	Trp	Thr	Ile	Leu	Arg	Asp	Arg	Gly	Ser	Phe	Glu	Asp
	705				710				715				720			
	Ser	Thr	Thr	Arg	Phe	Tyr	Thr	Ala	Cys	Val	Val	Glu	Ala	Phe	Ala	Tyr
				725				730					735			
50	Leu	His	Ser	Lys	Gly	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu
			740					745					750			
	Ile	Leu	Asp	His	Arg	Gly	Tyr	Ala	Lys	Leu	Val	Asp	Phe	Gly	Phe	Ala
		755				760						765				
55	Lys	Lys	Ile	Gly	Phe	Gly	Lys	Lys	Thr	Trp	Thr	Phe	Cys	Gly	Thr	Pro
		770				775					780					
	Glu	Tyr	Val	Ala	Pro	Glu	Ile	Ile	Leu	Asn	Lys	Gly	His	Asp	Ile	Ser

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[illegible]

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...2795
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

	ATG	GGC	ACC	TTG	CGG	GAT	TTA	CAG	TAC	GCG	CTC	CAG	GAG	AAG	ATC	GAG	48
	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	Ala	Leu	Gln	Glu	Lys	Ile	Glu	
40	1				5					10					15		
	GAG	CTG	AGG	CAG	CGG	GAT	GCT	CTC	ATC	GAC	GAG	CTG	GAG	CTG	GAG	TTG	96
	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	Asp	Glu	Leu	Glu	Leu	Glu	Leu	
				20					25					30			
45	GAT	CAG	AAG	GAC	GAA	CTG	ATC	CAG	AAG	CTG	CAG	AAC	GAG	CTG	GAC	AAG	144
	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Lys	
			35					40					45				
50	TAC	CGC	TCG	GTG	ATC	CGA	CCA	GCC	ACC	CAG	CAG	GCG	CAG	AAG	CAG	AGC	192
	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	Gln	Gln	Ala	Gln	Lys	Gln	Ser	
		50					55					60					
55	GCG	AGC	ACC	TTG	CAG	GGC	GAG	CCG	CGC	ACC	AAG	CGG	CAG	GCG	ATC	TCC	240
	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	Thr	Lys	Arg	Gln	Ala	Ile	Ser	
	65					70					75				80		

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	GCC GAG CCC ACC GCC TTC GAC ATC CAG GAT CTC AGC CAT GTG ACC CTG	288
	Ala Glu Pro Thr Ala Phe Asp Ile Gln Asp Leu Ser His Val Thr Leu	
	85 90 95	
5	CCC TTC TAC CCC AAG AGC CCA CAG TCC AAG GAT CTT ATA AAG GAA GCT	336
	Pro Phe Tyr Pro Lys Ser Pro Gln Ser Lys Asp Leu Ile Lys Glu Ala	
	100 105 110	
10	ATC CTT GAC AAT GAC TTT ATG AAG AAC TTG GAG CTG TCG CAG ATC CAG	384
	Ile Leu Asp Asn Asp Phe Met Lys Asn Leu Glu Leu Ser Gln Ile Gln	
	115 120 125	
15	GAG ATT GTG GAT TGT ATG TAC CCG GTG GAG TAT GGC AAG GAC AGT TGC	432
	Glu Ile Val Asp Cys Met Tyr Pro Val Glu Tyr Gly Lys Asp Ser Cys	
	130 135 140	
20	ATC ATC AAA GAA GGA GAC GTG GGG TCA CTG GTG TAT GTC ATG GAA GAT	480
	Ile Ile Lys Glu Gly Asp Val Gly Ser Leu Val Tyr Val Met Glu Asp	
	145 150 155 160	
25	GGT AAG GTT GAA GTT ACA AAA GAA GGT GTG AAG TTG TGT ACC ATG GGT	528
	Gly Lys Val Glu Val Thr Lys Glu Gly Val Lys Leu Cys Thr Met Gly	
	165 170 175	
	CCA GGA AAA GTG TTT GGG GAA TTG GCT ATT CTT TAC AAC TGT ACC CGG	576
	Pro Gly Lys Val Phe Gly Glu Leu Ala Ile Leu Tyr Asn Cys Thr Arg	
	180 185 190	
30	ACA GCG ACC GTC AAG ACT CTT GTA AAT GTA AAA CTC TGG GCC ATT GAT	624
	Thr Ala Thr Val Lys Thr Leu Val Asn Val Lys Leu Trp Ala Ile Asp	
	195 200 205	
35	CGA CAA TGT TTT CAA ACA ATA ATG ATG AGG ACA GGA CTC ATC AAG CAT	672
	Arg Gln Cys Phe Gln Thr Ile Met Met Arg Thr Gly Leu Ile Lys His	
	210 215 220	
40	ACC GAG TAT ATG GAA TTT TTA AAA AGC GTT CCA ACA TTC CAG AGC CTT	720
	Thr Glu Tyr Met Glu Phe Leu Lys Ser Val Pro Thr Phe Gln Ser Leu	
	225 230 235 240	
45	CCT GAA GAG ATC CTC AGC AAG CTT GCT GAT GTC CTT GAA GAG ACC CAC	768
	Pro Glu Glu Ile Leu Ser Lys Leu Ala Asp Val Leu Glu Glu Thr His	
	245 250 255	
	TAT GAA AAT GGA GAA TAT ATT ATC AGG CAA GGT GCA AGA GGG GAC ACC	816
	Tyr Glu Asn Gly Glu Tyr Ile Ile Arg Gln Gly Ala Arg Gly Asp Thr	
	260 265 270	
50	TTC TTT ATC ATC AGC AAA GGA ACG GTA AAT GTC ACT CGT GAA GAC TCA	864
	Phe Phe Ile Ile Ser Lys Gly Thr Val Asn Val Thr Arg Glu Asp Ser	
	275 280 285	
55	CCG AGT GAA GAC CCA GTC TTT CTT AGA ACT TTA GGA AAA GGA GAC TGG	912
	Pro Ser Glu Asp Pro Val Phe Leu Arg Thr Leu Gly Lys Gly Asp Trp	
	290 295 300	

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5	TTT GGA GAG AAA GCC TTG CAG GGG GAA GAT GTG AGA ACA GCA AAC GTA	960
	Phe Gly Glu Lys Ala Leu Gln Gly Glu Asp Val Arg Thr Ala Asn Val	
	305 310 315 320	
10	ATT GCT GCA GAA GCT GTA ACC TGC CTT GTG ATT GAC AGA GAC TCT TTT	1008
	Ile Ala Ala Glu Ala Val Thr Cys Leu Val Ile Asp Arg Asp Ser Phe	
	325 330 335	
15	AAA CAT TTG ATT GGA GGG CTG GAT GAT GTT TCT AAT AAA GCA TAT GAA	1056
	Lys His Leu Ile Gly Gly Leu Asp Asp Val Ser Asn Lys Ala Tyr Glu	
	340 345 350	
20	GAT GCA GAA GCT AAA GCA AAA TAT GAA GCT GAA GCG GCT TTC TTC GCC	1104
	Asp Ala Glu Ala Lys Ala Lys Tyr Glu Ala Glu Ala Phe Phe Ala	
	355 360 365	
25	AAC CTG AAG CTG TCT GAT TTC AAC ATC ATT GAT ACC CTT GGA GTT GGA	1152
	Asn Leu Lys Leu Ser Asp Phe Asn Ile Ile Asp Thr Leu Gly Val Gly	
	370 375 380	
30	GGT TTC GGA CGA GTA GAA CTG GTC CAG TTG AAA AGT GAA GAA TCC AAA	1200
	Gly Phe Gly Arg Val Glu Leu Val Gln Leu Lys Ser Glu Glu Ser Lys	
	385 390 395 400	
35	ACG TTT GCA ATG AAG ATT CTC AAG AAA CGT CAC ATT GTG GAC ACA AGA	1248
	Thr Phe Ala Met Lys Ile Leu Lys Lys Arg His Ile Val Asp Thr Arg	
	405 410 415	
40	CAG CAG GAG CAC ATC CGC TCA GAG AAG CAG ATC ATG CAG GGG GCT CAT	1296
	Gln Gln Glu His Ile Arg Ser Glu Lys Gln Ile Met Gln Gly Ala His	
	420 425 430	
45	TCC GAT TTC ATA GTG AGA CTG TAC AGA ACA TTT AAG GAC AGC AAA TAT	1344
	Ser Asp Phe Ile Val Arg Leu Tyr Arg Thr Phe Lys Asp Ser Lys Tyr	
	435 440 445	
50	TTG TAT ATG TTG ATG GAA GCT TGT CTA GGT GGA GAG CTC TGG ACC ATT	1392
	Leu Tyr Met Leu Met Glu Ala Cys Leu Gly Gly Glu Leu Trp Thr Ile	
	450 455 460	
55	CTC AGG GAT AGA GGT TCG TTT GAA GAT TCT ACA ACC AGA TTT TAC ACA	1440
	Leu Arg Asp Arg Gly Ser Phe Glu Asp Ser Thr Thr Arg Phe Tyr Thr	
	465 470 475 480	
60	GCA TGT GTG GTA GAA GCT TTT GCC TAT CTG CAT TCC AAA GGA ATC ATT	1488
	Ala Cys Val Val Glu Ala Phe Ala Tyr Leu His Ser Lys Gly Ile Ile	
	485 490 495	
65	TAC AGG GAC CTC AAG CCA GAA AAT CTC ATC CTA GAT CAC CGA GGT TAT	1536
	Tyr Arg Asp Leu Lys Pro Glu Asn Leu Ile Leu Asp His Arg Gly Tyr	
	500 505 510	
70	GCC AAA CTG GTT GAT TTT GGC TTT GCA AAG AAA ATA GGA TTT GGA AAG	1584
	Ala Lys Leu Val Asp Phe Gly Phe Ala Lys Lys Ile Gly Phe Gly Lys	
	515 520 525	

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	AAA	ACA	TGG	ACT	TTT	TGT	GGG	ACT	CCA	GAG	TAT	GTA	GCC	CCA	GAG	ATC	1632
	Lys	Thr	Trp	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Val	Ala	Pro	Glu	Ile	
	530						535					540					
5	ATC	CTG	AAC	AAA	GGC	CAT	GAC	ATT	TCA	GCC	GAC	TAC	TGG	TCA	CTG	GGA	1680
	Ile	Leu	Asn	Lys	Gly	His	Asp	Ile	Ser	Ala	Asp	Tyr	Trp	Ser	Leu	Gly	
	545					550					555					560	
10	ATC	CTA	ATG	TAT	GAA	CTC	CTG	ACT	GGC	AGC	CCA	CCT	TTC	TCA	GGC	CCA	1728
	Ile	Leu	Met	Tyr	Glu	Leu	Leu	Thr	Gly	Ser	Pro	Pro	Phe	Ser	Gly	Pro	
					565					570					575		
15	GAT	CCT	ATG	AAA	ACC	TAT	AAC	ATC	ATA	TTG	AGG	GGG	ATT	GAC	ATG	ATA	1776
	Asp	Pro	Met	Lys	Thr	Tyr	Asn	Ile	Ile	Leu	Arg	Gly	Ile	Asp	Met	Ile	
				580					585					590			
20	GAA	TTT	CCA	AAG	AAG	ATT	GCC	AAA	AAT	GCT	GCT	AAT	TTA	ATT	AAA	AAA	1824
	Glu	Phe	Pro	Lys	Lys	Ile	Ala	Lys	Asn	Ala	Ala	Asn	Leu	Ile	Lys	Lys	
			595					600					605				
25	CTA	TGC	AGG	GAC	AAT	CCA	TCA	GAA	AGA	TTA	GGG	AAT	TTG	AAA	AAT	GGA	1872
	Leu	Cys	Arg	Asp	Asn	Pro	Ser	Glu	Arg	Leu	Gly	Asn	Leu	Lys	Asn	Gly	
	610						615					620					
30	GTA	AAA	GAC	ATT	CAA	AAG	CAC	AAA	TGG	TTT	GAG	GGC	TTT	AAC	TGG	GAA	1920
	Val	Lys	Asp	Ile	Gln	Lys	His	Lys	Trp	Phe	Glu	Gly	Phe	Asn	Trp	Glu	
	625					630					635					640	
35	GGC	TTA	AGA	AAA	GGT	ACC	TTG	ACA	CCT	CCT	ATA	ATA	CCA	AGT	GTT	GCA	1968
	Gly	Leu	Arg	Lys	Gly	Thr	Leu	Thr	Pro	Pro	Ile	Ile	Pro	Ser	Val	Ala	
					645					650					655		
40	TCA	CCC	ACA	GAC	ACA	AGT	AAT	TTT	GAC	AGT	TTC	CCT	GAG	GAC	AAC	GAT	2016
	Ser	Pro	Thr	Asp	Thr	Ser	Asn	Phe	Asp	Ser	Phe	Pro	Glu	Asp	Asn	Asp	
				660					665					670			
45	GAA	CCA	CCA	CCT	GAT	GAC	AAC	TCA	GGA	TGG	GAT	ATA	GAC	TTC	TCG	GAT	2064
	Glu	Pro	Pro	Pro	Asp	Asp	Asn	Ser	Gly	Trp	Asp	Ile	Asp	Phe	Ser	Asp	
			675					680					685				
50	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	2112
	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	
	690						695					700					
55	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	2160
	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	
	705					710					715					720	
60	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	2208
	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	
					725					730					735		
65	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	2256
	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	
				740					745					750			

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	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC	2304
	Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr	
	755 760 765	
5	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA	2352
	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	
	770 775 780	
10	GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC	2400
	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr	
	785 790 795 800	
15	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC	2448
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	
	805 810 815	
20	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG	2496
	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly	
	820 825 830	
25	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC	2544
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala	
	835 840 845	
30	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC	2592
	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
	850 855 860	
35	ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC	2640
	Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr	
	865 870 875 880	
40	CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC	2688
	Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser	
	885 890 895	
45	ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG	2736
	Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met	
	900 905 910	
50	GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC	2784
	Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp	
	915 920 925	
55	GAG CTG TAC AA GTAA	2799
	Glu Leu Tyr Lys	
	930	

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 932 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	Ala	Leu	Gln	Glu	Lys	Ile	Glu
	1				5					10					15	
10	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	Asp	Glu	Leu	Glu	Leu	Glu	Leu
				20					25					30		
	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Lys
			35					40					45			
	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	Gln	Gln	Ala	Gln	Lys	Gln	Ser
15		50					55					60				
	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	Thr	Lys	Arg	Gln	Ala	Ile	Ser
	65					70					75					80
	Ala	Glu	Pro	Thr	Ala	Phe	Asp	Ile	Gln	Asp	Leu	Ser	His	Val	Thr	Leu
				85						90					95	
20	Pro	Phe	Tyr	Pro	Lys	Ser	Pro	Gln	Ser	Lys	Asp	Leu	Ile	Lys	Glu	Ala
				100					105					110		
	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn	Leu	Glu	Leu	Ser	Gln	Ile	Gln
			115						120					125		
	Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val	Glu	Tyr	Gly	Lys	Asp	Ser	Cys
25			130					135				140				
	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser	Leu	Val	Tyr	Val	Met	Glu	Asp
	145					150					155				160	
	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly	Val	Lys	Leu	Cys	Thr	Met	Gly
				165						170					175	
30	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala	Ile	Leu	Tyr	Asn	Cys	Thr	Arg
				180						185				190		
	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn	Val	Lys	Leu	Trp	Ala	Ile	Asp
			195					200					205			
	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met	Arg	Thr	Gly	Leu	Ile	Lys	His
35			210					215				220				
	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser	Val	Pro	Thr	Phe	Gln	Ser	Leu
	225					230					235				240	
	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala	Asp	Val	Leu	Glu	Glu	Thr	His
				245						250					255	
40	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	Gln	Gly	Ala	Arg	Gly	Asp	Thr
			260						265					270		
	Phe	Phe	Ile	Ser	Lys	Gly	Thr	Val	Asn	Val	Thr	Arg	Glu	Asp	Ser	
			275					280				285				
	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg	Thr	Leu	Gly	Lys	Gly	Asp	Trp
45			290				295					300				
	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu	Asp	Val	Arg	Thr	Ala	Asn	Val
	305					310					315				320	
	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu	Val	Ile	Asp	Arg	Asp	Ser	Phe
				325						330					335	
50	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp	Val	Ser	Asn	Lys	Ala	Tyr	Glu
			340					345					350			
	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu	Ala	Glu	Ala	Ala	Phe	Phe	Ala
			355					360				365				
	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile	Ile	Asp	Thr	Leu	Gly	Val	Gly
55			370				375					380				
	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln	Leu	Lys	Ser	Glu	Glu	Ser	Lys

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	385		390		395		400
	Thr	Phe	Ala	Met	Lys	Ile	Leu
					405		
	Gln	Gln	Glu	His	Ile	Arg	Ser
5					420		
	Ser	Asp	Phe	Ile	Val	Arg	Leu
					435		
	Leu	Tyr	Met	Leu	Met	Glu	Ala
					450		
10	Leu	Arg	Asp	Arg	Gly	Ser	Phe
					465		
	Ala	Cys	Val	Val	Glu	Ala	Phe
					485		
	Tyr	Arg	Asp	Leu	Lys	Pro	Glu
15					500		
	Ala	Lys	Leu	Val	Asp	Phe	Gly
					515		
	Lys	Thr	Trp	Thr	Phe	Cys	Gly
					530		
20	Ile	Leu	Asn	Lys	Gly	His	Asp
					545		
	Ile	Leu	Met	Tyr	Glu	Leu	Leu
					565		
25	Asp	Pro	Met	Lys	Thr	Tyr	Asn
					580		
	Glu	Phe	Pro	Lys	Lys	Ile	Ala
					595		
	Leu	Cys	Arg	Asp	Asn	Pro	Ser
					610		
30	Val	Lys	Asp	Ile	Gln	Lys	His
					625		
	Gly	Leu	Arg	Lys	Gly	Thr	Leu
					645		
35	Ser	Pro	Thr	Asp	Thr	Ser	Asn
					660		
	Glu	Pro	Pro	Pro	Asp	Asp	Asn
					675		
	Pro	Pro	Val	Ala	Thr	Met	Val
					690		
40	Val	Val	Pro	Ile	Leu	Val	Glu
					705		
	Phe	Ser	Val	Ser	Gly	Glu	Gly
					725		
45	Thr	Leu	Lys	Phe	Ile	Cys	Thr
					740		
	Thr	Leu	Val	Thr	Thr	Leu	Thr
					755		
	Pro	Asp	His	Met	Lys	Gln	His
					770		
50	Gly	Tyr	Val	Gln	Glu	Arg	Thr
					785		
	Lys	Thr	Arg	Ala	Glu	Val	Lys
					805		
	Ile	Glu	Leu	Lys	Gly	Ile	Asp
55					820		
	His	Lys	Leu	Glu	Tyr	Asn	Tyr
					825		

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835 840 845
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
 850 855 860
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 5 865 870 875 880
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 885 890 895
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 900 905 910
 10 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 915 920 925
 Glu Leu Tyr Lys
 930

15 (2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2184 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2181

(D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336

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	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
5	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
10	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					
15	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
20	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
25	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185						190			
30	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
35	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
40	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
45	GGA	CTC	AGA	TCT	CGA	GGC	ACC	ATG	AGC	GAC	GTG	GCT	ATT	GTG	AAG	GAG	768
	Gly	Leu	Arg	Ser	Arg	Gly	Thr	Met	Ser	Asp	Val	Ala	Ile	Val	Lys	Glu	
					245					250					255		
50	GGT	TGG	CTG	CAC	AAA	CGA	GGG	GAG	TAC	ATC	AAG	ACC	TGG	CGG	CCA	CGC	816
	Gly	Trp	Leu	His	Lys	Arg	Gly	Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	
				260				265					270				
55	TAC	TTC	CTC	CTC	AAG	AAT	GAT	GGC	ACC	TTC	ATT	GGC	TAC	AAG	GAG	CGG	864
	Tyr	Phe	Leu	Leu	Lys	Asn	Asp	Gly	Thr	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	
			275					280					285				
60	CCG	CAG	GAT	GTG	GAC	CAA	CGT	GAG	GCT	CCC	CTC	AAC	AAC	TTC	TCT	GTG	912
	Pro	Gln	Asp	Val	Asp	Gln	Arg	Glu	Ala	Pro	Leu	Asn	Asn	Phe	Ser	Val	
		290					295					300					
65	GCG	CAG	TGC	CAG	CTG	ATG	AAG	ACG	GAG	CGG	CCC	CGG	CCC	AAC	ACC	TTC	960
	Ala	Gln	Cys	Gln	Leu	Met	Lys	Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	
	305					310					315					320	
70	ATC	ATC	CGC	TGC	CTG	CAG	TGG	ACC	ACT	GTC	ATC	GAA	CGC	ACC	TTC	CAT	1008

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	Ile	Ile	Arg	Cys	Leu	Gln	Trp	Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	
					325					330					335		
5	GTG	GAG	ACT	CCT	GAG	GAG	CGG	GAG	GAG	TGG	ACA	ACC	GCC	ATC	CAG	ACT	1056
	Val	Glu	Thr	Pro	Glu	Glu	Arg	Glu	Glu	Trp	Thr	Thr	Ala	Ile	Gln	Thr	
				340				345					350				
10	GTG	GCT	GAC	GGC	CTC	AAG	AAG	CAG	GAG	GAG	GAG	GAG	ATG	GAC	TTC	CGG	1104
	Val	Ala	Asp	Gly	Leu	Lys	Lys	Gln	Glu	Glu	Glu	Glu	Met	Asp	Phe	Arg	
			355				360					365					
15	TCG	GGC	TCA	CCC	AGT	GAC	AAC	TCA	GGG	GCT	GAA	GAG	ATG	GAG	GTG	TCC	1152
	Ser	Gly	Ser	Pro	Ser	Asp	Asn	Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser	
		370					375				380						
20	CTG	GCC	AAG	CCC	AAG	CAC	CGC	GTG	ACC	ATG	AAC	GAG	TTT	GAG	TAC	CTG	1200
	Leu	Ala	Lys	Pro	Lys	His	Arg	Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	
		385				390					395				400		
25	AAG	CTG	CTG	GGC	AAG	GGC	ACT	TTC	GGC	AAG	GTG	ATC	CTG	GTG	AAG	GAG	1248
	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	
				405					410						415		
30	AAG	GCC	ACA	GGC	CGC	TAC	TAC	GCC	ATG	AAG	ATC	CTC	AAG	AAG	GAA	GTC	1296
	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	
			420					425						430			
35	ATC	GTG	GCC	AAG	GAC	GAG	GTG	GCC	CAC	ACA	CTC	ACC	GAG	AAC	CGC	GTC	1344
	Ile	Val	Ala	Lys	Asp	Glu	Val	Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	
			435				440						445				
40	CTG	CAG	AAC	TCC	AGG	CAC	CCC	TTC	CTC	ACA	GCC	CTG	AAG	TAC	TCT	TTC	1392
	Leu	Gln	Asn	Ser	Arg	His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	
		450					455					460					
45	CAG	ACC	CAC	GAC	CGC	CTC	TGC	TTT	GTC	ATG	GAG	TAC	GCC	AAC	GGG	GGC	1440
	Gln	Thr	His	Asp	Arg	Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	
		465				470				475					480		
50	GAG	CTG	TTC	TTC	CAC	CTG	TCC	CGG	GAA	CGT	GTG	TTC	TCC	GAG	GAC	CGG	1488
	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	
					485			490						495			
55	GCC	CGC	TTC	TAT	GGC	GCT	GAG	ATT	GTG	TCA	GCC	CTG	GAC	TAC	CTG	CAC	1536
	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His	
			500					505					510				
60	TCG	GAG	AAG	AAC	GTG	GTG	TAC	CGG	GAC	CTC	AAG	CTG	GAG	AAC	CTC	ATG	1584
	Ser	Glu	Lys	Asn	Val	Val	Tyr	Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	
			515				520					525					
65	CTG	GAC	AAG	GAC	GGG	CAC	ATT	AAG	ATC	ACA	GAC	TTC	GGG	CTG	TGC	AAG	1632
	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	
		530					535					540					
70	GAG	GGG	ATC	AAG	GAC	GGT	GCC	ACC	ATG	AAG	ACC	TTT	TGC	GGC	ACA	CCT	1680

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	Glu	Gly	Ile	Lys	Asp	Gly	Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	
	545					550					555					560	
5	GAG	TAC	CTG	GCC	CCC	GAG	GTG	CTG	GAG	GAC	AAT	GAC	TAC	GGC	CGT	GCA	1728
	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	
				565					570					575			
10	GTG	GAC	TGG	TGG	GGG	CTG	GGC	GTG	GTC	ATG	TAC	GAG	ATG	ATG	TGC	GGT	1776
	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	
				580					585					590			
15	CGC	CTG	CCC	TTC	TAC	AAC	CAG	GAC	CAT	GAG	AAG	CTT	TTT	GAG	CTC	ATC	1824
	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	
			595				600						605				
	CTC	ATG	GAG	GAG	ATC	CGC	TTC	CCG	CGC	ACG	CTT	GGT	CCC	GAG	GCC	AAG	1872
	Leu	Met	Glu	Glu	Ile	Arg	Phe	Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys	
		610					615					620					
20	TCC	TTG	CTT	TCA	GGG	CTG	CTC	AAG	AAG	GAC	CCC	AAG	CAG	AGG	CTT	GGC	1920
	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	
		625				630					635					640	
25	GGG	GGC	TCC	GAG	GAC	GCC	AAG	GAG	ATC	ATG	CAG	CAT	CGC	TTC	TTT	GCC	1968
	Gly	Gly	Ser	Glu	Asp	Ala	Lys	Glu	Ile	Met	Gln	His	Arg	Phe	Phe	Ala	
				645						650					655		
30	GGT	ATC	GTG	TGG	CAG	CAC	GTG	TAC	GAG	AAG	AAG	CTC	AGC	CCA	CCC	TTC	2016
	Gly	Ile	Val	Trp	Gln	His	Val	Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe	
				660					665					670			
35	AAG	CCC	CAG	GTC	ACG	TCG	GAG	ACT	GAC	ACC	AGG	TAT	TTT	GAT	GAG	GAG	2064
	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	
			675				680						685				
	TTC	ACG	GCC	CAG	ATG	ATC	ACC	ATC	ACA	CCA	CCT	GAC	CAA	GAT	GAC	AGC	2112
	Phe	Thr	Ala	Gln	Met	Ile	Thr	Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser	
			690				695					700					
40	ATG	GAG	TGT	GTG	GAC	AGC	GAG	CGC	AGG	CCC	CAC	TTC	CCC	CAG	TTC	TCC	2160
	Met	Glu	Cys	Val	Asp	Ser	Glu	Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	
		705				710				715						720	
45	TAC	TCG	GCC	AGC	AGC	ACG	GCC	TGA									2184
	Tyr	Ser	Ala	Ser	Ser	Thr	Ala										
				725													

(2) INFORMATION FOR SEQ ID NO:139:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

287

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

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5      Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
      1          5          10          15
      Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
      20          25          30
10     Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
      35          40          45
      Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50          55          60
      Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
15     65          70          75          80
      Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
      85          90          95
      Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
      100         105         110
20     Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
      115         120         125
      Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
      130         135         140
      Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
25     145         150         155         160
      Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
      165         170         175
      Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
      180         185         190
30     Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
      195         200         205
      Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
      210         215         220
      Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
35     225         230         235         240
      Gly Leu Arg Ser Arg Gly Thr Met Ser Asp Val Ala Ile Val Lys Glu
      245         250         255
      Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro Arg
      260         265         270
40     Tyr Phe Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg
      275         280         285
      Pro Gln Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn Phe Ser Val
      290         295         300
      Ala Gln Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe
45     305         310         315         320
      Ile Ile Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His
      325         330         335
      Val Glu Thr Pro Glu Glu Arg Glu Glu Trp Thr Thr Ala Ile Gln Thr
      340         345         350
50     Val Ala Asp Gly Leu Lys Lys Gln Glu Glu Glu Glu Met Asp Phe Arg
      355         360         365
      Ser Gly Ser Pro Ser Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser
      370         375         380
      Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu
55     385         390         395         400
      Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu

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				405					410					415		
	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val
				420					425					430		
	Ile	Val	Ala	Lys	Asp	Glu	Val	Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val
5			435					440					445			
	Leu	Gln	Asn	Ser	Arg	His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe
			450				455					460				
	Gln	Thr	His	Asp	Arg	Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly
	465					470				475					480	
10	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg
				485					490					495		
	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His
			500				505					510				
	Ser	Glu	Lys	Asn	Val	Val	Tyr	Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met
15			515				520					525				
	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys
		530				535					540					
	Glu	Gly	Ile	Lys	Asp	Gly	Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro
	545				550				555						560	
20	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala
				565					570						575	
	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly
			580				585					590				
	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile
25			595				600					605				
	Leu	Met	Glu	Glu	Ile	Arg	Phe	Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys
		610				615					620					
	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly
	625				630				635						640	
30	Gly	Gly	Ser	Glu	Asp	Ala	Lys	Glu	Ile	Met	Gln	His	Arg	Phe	Phe	Ala
				645					650					655		
	Gly	Ile	Val	Trp	Gln	His	Val	Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe
			660				665					670				
	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu
35			675				680					685				
	Phe	Thr	Ala	Gln	Met	Ile	Thr	Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser
		690				695					700					
	Met	Glu	Cys	Val	Asp	Ser	Glu	Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser
	705				710				715						720	
40	Tyr	Ser	Ala	Ser	Ser	Thr	Ala									
				725												

(2) INFORMATION FOR SEQ ID NO:140:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...2391
 - (D) OTHER INFORMATION:
- 55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

5	ATG GAC GAA CTG TTC CCC CTC ATC TTC CCG GCA GAG CCA GCC CAG GCC	48
	Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala	
	1 5 10 15	
10	TCT GGC CCC TAT GTG GAG ATC ATT GAG CAG CCC AAG CAG CGG GGC ATG	96
	Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met	
	20 25 30	
15	CGC TTC CGC TAC AAG TGC GAG GGG CGC TCC GCG GGC AGC ATC CCA GGC	144
	Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly	
	35 40 45	
20	GAG AGG AGC ACA GAT ACC ACC AAG ACC CAC CCC ACC ATC AAG ATC AAT	192
	Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn	
	50 55 60	
25	GGC TAC ACA GGA CCA GGG ACA GTG CGC ATC TCC CTG GTC ACC AAG GAC	240
	Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp	
	65 70 75 80	
30	CCT CCT CAC CGG CCT CAC CCC CAC GAG CTT GTA GGA AAG GAC TGC CGG	288
	Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg	
	85 90 95	
35	GAT GGC TTC TAT GAG GCT GAG CTC TGC CCG GAC CGC TGC ATC CAC AGT	336
	Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser	
	100 105 110	
40	TTC CAG AAC CTG GGA ATC CAG TGT GTG AAG AAG CGG GAC CTG GAG CAG	384
	Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln	
	115 120 125	
45	GCT ATC AGT CAG CGC ATC CAG ACC AAC AAC AAC CCC TTC CAA GTT CCT	432
	Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro	
	130 135 140	
50	ATA GAA GAG CAG CGT GGG GAC TAC GAC CTG AAT GCT GTG CGG CTC TGC	480
	Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys	
	145 150 155 160	
55	TTC CAG GTG ACA GTG CGG GAC CCA TCA GGC AGG CCC CTC CGC CTG CCG	528
	Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro	
	165 170 175	
60	CCT GTC CTT CCT CAT CCC ATC TTT GAC AAT CGT GCC CCC AAC ACT GCC	576
	Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala	
	180 185 190	
65	GAG CTC AAG ATC TGC CGA GTG AAC CGA AAC TCT GGC AGC TGC CTC GGT	624
	Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly	
	195 200 205	
70	GGG GAT GAG ATC TTC CTA CTG TGT GAC AAG GTG CAG AAA GAG GAC ATT	672

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	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Glu	Asp	Ile	
	210						215					220					
5	GAG	GTG	TAT	TTC	ACG	GGA	CCA	GGC	TGG	GAG	GCC	CGA	GGC	TCC	TTT	TCG	720
	Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	Ala	Arg	Gly	Ser	Phe	Ser	
	225					230				235						240	
10	CAA	GCT	GAT	GTG	CAC	CGA	CAA	GTG	GCC	ATT	GTG	TTC	CGG	ACC	CCT	CCC	768
	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro	
					245				250						255		
15	TAC	GCA	GAC	CCC	AGC	CTG	CAG	GCT	CCT	GTG	CGT	GTC	TCC	ATG	CAG	CTG	816
	Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val	Arg	Val	Ser	Met	Gln	Leu	
				260				265						270			
20	CGG	CGG	CCT	TCC	GAC	CGG	GAG	CTC	AGT	GAG	CCC	ATG	GAA	TTC	CAG	TAC	864
	Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu	Pro	Met	Glu	Phe	Gln	Tyr	
			275				280					285					
25	CTG	CCA	GAT	ACA	GAC	GAT	CGT	CAC	CGG	ATT	GAG	GAG	AAA	CGT	AAA	AGG	912
	Leu	Pro	Asp	Thr	Asp	Asp	Arg	His	Arg	Ile	Glu	Glu	Lys	Arg	Lys	Arg	
	290					295					300						
30	ACA	TAT	GAG	ACC	TTC	AAG	AGC	ATC	ATG	AAG	AAG	AGT	CCT	TTC	AGC	GGA	960
	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	Lys	Ser	Pro	Phe	Ser	Gly	
	305				310				315							320	
35	CCC	ACC	GAC	CCC	CGG	CCT	CCA	CCT	CGA	CGC	ATT	GCT	GTG	CCT	TCC	CGC	1008
	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg	Ile	Ala	Val	Pro	Ser	Arg	
				325					330					335			
40	AGC	TCA	GCT	TCT	GTC	CCC	AAG	CCA	GCA	CCC	CAG	CCC	TAT	CCC	TTT	ACG	1056
	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	Gln	Pro	Tyr	Pro	Phe	Thr	
				340				345					350				
45	TCA	TCC	CTG	AGC	ACC	ATC	AAC	TAT	GAT	GAG	TTT	CCC	ACC	ATG	GTG	TTT	1104
	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	Phe	Pro	Thr	Met	Val	Phe	
			355				360					365					
50	CCT	TCT	GGG	CAG	ATC	AGC	CAG	GCC	TCG	GCC	TTG	GCC	CCG	GCC	CCT	CCC	1152
	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	Leu	Ala	Pro	Ala	Pro	Pro	
	370					375					380						
55	CAA	GTC	CTG	CCC	CAG	GCT	CCA	GCC	CCT	GCC	CCT	GCT	CCA	GCC	ATG	GTA	1200
	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Met	Val	
	385				390				395						400		
60	TCA	GCT	CTG	GCC	CAG	GCC	CCA	GCC	CCT	GTC	CCA	GTC	CTA	GCC	CCA	GGC	1248
	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	Pro	Val	Leu	Ala	Pro	Gly	
				405					410					415			
65	CCT	CCT	CAG	GCT	GTG	GCC	CCA	CCT	GCC	CCC	AAG	CCC	ACC	CAG	GCT	GGG	1296
	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	Lys	Pro	Thr	Gln	Ala	Gly	
			420					425					430				
70	GAA	GGA	ACG	CTG	TCA	GAG	GCC	CTG	CTG	CAG	CTG	CAG	TTT	GAT	GAT	GAA	1344

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	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	Leu	Gln	Phe	Asp	Asp	Glu	
			435					440					445				
5	GAC	CTG	GGG	GCC	TTG	CTT	GGC	AAC	AGC	ACA	GAC	CCA	GCT	GTG	TTC	ACA	1392
	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr	Asp	Pro	Ala	Val	Phe	Thr	
		450					455					460					
10	GAC	CTG	GCA	TCC	GTC	GAC	AAC	TCC	GAG	TTT	CAG	CAG	CTG	CTG	AAC	CAG	1440
	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	Gln	Gln	Leu	Leu	Asn	Gln	
		465				470					475					480	
15	GGC	ATA	CCT	GTG	GCC	CCC	CAC	ACA	ACT	GAG	CCC	ATG	CTG	ATG	GAG	TAC	1488
	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	Pro	Met	Leu	Met	Glu	Tyr	
					485					490					495		
	CCT	GAG	GCT	ATA	ACT	CGC	CTA	GTG	ACA	GGG	GCC	CAG	AGG	CCC	CCC	GAC	1536
	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	Ala	Gln	Arg	Pro	Pro	Asp	
				500					505					510			
20	CCA	GCT	CCT	GCT	CCA	CTG	GGG	GCC	CCG	GGG	CTC	CCC	AAT	GGC	CTC	CTT	1584
	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly	Leu	Pro	Asn	Gly	Leu	Leu	
				515				520					525				
25	TCA	GGA	GAT	GAA	GAC	TTC	TCC	TCC	ATT	GCG	GAC	ATG	GAC	TTC	TCA	GCC	1632
	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala	Asp	Met	Asp	Phe	Ser	Ala	
		530					535					540					
30	CTG	CTG	AGT	CAG	ATC	AGC	TCC	TTG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	1680
	Leu	Leu	Ser	Gln	Ile	Ser	Ser	Leu	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	
		545				550					555					560	
35	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	1728
	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
				565						570					575		
	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	1776
	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
				580				585						590			
40	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	1824
	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	
			595				600						605				
45	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	1872
	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	
			610				615					620					
50	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	1920
	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	
		625				630					635					640	
55	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	1968
	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	
				645						650					655		
	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	2016

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	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	
				660				665						670			
5	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	2064
	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	
			675					680					685				
10	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	2112
	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	
			690				695					700					
15	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	2160
	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	
			705			710					715				720		
	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	2208
	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	
					725					730					735		
20	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	2256
	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	
				740					745					750			
25	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	2304
	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	
			755					760					765				
30	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG	ACC	2352
	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	
			770				775					780					
35	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TAA			2394
	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys				
			785			790					795						

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

50	Met	Asp	Glu	Leu	Phe	Pro	Leu	Ile	Phe	Pro	Ala	Glu	Pro	Ala	Gln	Ala
	1				5				10					15		
	Ser	Gly	Pro	Tyr	Val	Glu	Ile	Ile	Glu	Gln	Pro	Lys	Gln	Arg	Gly	Met
				20				25					30			
	Arg	Phe	Arg	Tyr	Lys	Cys	Glu	Gly	Arg	Ser	Ala	Gly	Ser	Ile	Pro	Gly
55			35				40					45				
	Glu	Arg	Ser	Thr	Asp	Thr	Thr	Lys	Thr	His	Pro	Thr	Ile	Lys	Ile	Asn

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	50		55		60												
	Gly	Tyr	Thr	Gly	Pro	Gly	Thr	Val	Arg	Ile	Ser	Leu	Val	Thr	Lys	Asp	
	65					70					75					80	
5	Pro	Pro	His	Arg	Pro	His	Pro	His	Glu	Leu	Val	Gly	Lys	Asp	Cys	Arg	
					85					90					95		
	Asp	Gly	Phe	Tyr	Glu	Ala	Glu	Leu	Cys	Pro	Asp	Arg	Cys	Ile	His	Ser	
				100					105					110			
	Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Arg	Asp	Leu	Glu	Gln	
			115					120					125				
10	Ala	Ile	Ser	Gln	Arg	Ile	Gln	Thr	Asn	Asn	Asn	Pro	Phe	Gln	Val	Pro	
	130						135					140					
	Ile	Glu	Glu	Gln	Arg	Gly	Asp	Tyr	Asp	Leu	Asn	Ala	Val	Arg	Leu	Cys	
	145				150					155					160		
	Phe	Gln	Val	Thr	Val	Arg	Asp	Pro	Ser	Gly	Arg	Pro	Leu	Arg	Leu	Pro	
15					165					170					175		
	Pro	Val	Leu	Pro	His	Pro	Ile	Phe	Asp	Asn	Arg	Ala	Pro	Asn	Thr	Ala	
				180					185					190			
	Glu	Leu	Lys	Ile	Cys	Arg	Val	Asn	Arg	Asn	Ser	Gly	Ser	Cys	Leu	Gly	
			195					200				205					
20	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Glu	Asp	Ile	
	210						215					220					
	Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	Ala	Arg	Gly	Ser	Phe	Ser	
	225				230					235					240		
	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro	
25					245					250					255		
	Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val	Arg	Val	Ser	Met	Gln	Leu	
				260					265					270			
	Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu	Pro	Met	Glu	Phe	Gln	Tyr	
			275				280					285					
30	Leu	Pro	Asp	Thr	Asp	Asp	Arg	His	Arg	Ile	Glu	Glu	Lys	Arg	Lys	Arg	
	290						295					300					
	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	Lys	Ser	Pro	Phe	Ser	Gly	
	305				310						315				320		
	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg	Ile	Ala	Val	Pro	Ser	Arg	
35					325					330					335		
	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	Gln	Pro	Tyr	Pro	Phe	Thr	
				340					345					350			
	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	Phe	Pro	Thr	Met	Val	Phe	
			355				360					365					
40	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	Leu	Ala	Pro	Ala	Pro	Pro	
	370						375					380					
	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Met	Val	
	385				390						395				400		
	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	Pro	Val	Leu	Ala	Pro	Gly	
45					405					410					415		
	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	Lys	Pro	Thr	Gln	Ala	Gly	
				420					425					430			
	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	Leu	Gln	Phe	Asp	Asp	Glu	
			435				440					445					
50	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr	Asp	Pro	Ala	Val	Phe	Thr	
	450						455				460						
	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	Gln	Gln	Leu	Leu	Asn	Gln	
	465				470					475					480		
	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	Pro	Met	Leu	Met	Glu	Tyr	
55					485					490					495		
	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	Ala	Gln	Arg	Pro	Pro	Asp	

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		500		505		510
	Pro	Ala	Pro	Ala	Pro	Leu
		515		520		525
5	Ser	Gly	Asp	Glu	Asp	Phe
		530		535		540
	Leu	Leu	Ser	Gln	Ile	Ser
		545		550		555
	Ser	Lys	Gly	Glu	Glu	Leu
				565		570
10	Leu	Asp	Gly	Asp	Val	Asn
				580		585
	Glu	Gly	Asp	Ala	Thr	Tyr
				595		600
15	Thr	Gly	Lys	Leu	Pro	Val
				610		615
	Tyr	Gly	Val	Gln	Cys	Phe
				625		630
	Asp	Phe	Phe	Lys	Ser	Ala
				645		650
20	Ile	Phe	Phe	Lys	Asp	Asp
				660		665
	Phe	Glu	Gly	Asp	Thr	Leu
				675		680
25	Phe	Lys	Glu	Asp	Gly	Asn
				690		695
	Asn	Ser	His	Asn	Val	Tyr
				705		710
	Lys	Val	Asn	Phe	Lys	Ile
				725		730
30	Leu	Ala	Asp	His	Tyr	Gln
				740		745
	Leu	Leu	Pro	Asp	Asn	His
				755		760
35	Asp	Pro	Asn	Glu	Lys	Arg
				770		775
	Ala	Ala	Gly	Ile	Thr	Leu
				785		790

(2) INFORMATION FOR SEQ ID NO:142:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

50

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...2391
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

55

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG

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	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
5	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
10	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
15	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
20	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75						80	
25	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
30	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
35	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
40	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					
45	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150				155						160	
50	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
55	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185						190			
60	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
65	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
70	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720

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	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
5	GGA	CTC	AGA	TCT	CGA	GCC	ATG	GAC	GAA	CTG	TTC	CCC	CTC	ATC	TTC	CCG	768
	Gly	Leu	Arg	Ser	Arg	Ala	Met	Asp	Glu	Leu	Phe	Pro	Leu	Ile	Phe	Pro	
					245					250					255		
10	GCA	GAG	CCA	GCC	CAG	GCC	TCT	GGC	CCC	TAT	GTG	GAG	ATC	ATT	GAG	CAG	816
	Ala	Glu	Pro	Ala	Gln	Ala	Ser	Gly	Pro	Tyr	Val	Glu	Ile	Ile	Glu	Gln	
				260					265					270			
	CCC	AAG	CAG	CGG	GGC	ATG	CGC	TTC	CGC	TAC	AAG	TGC	GAG	GGG	CGC	TCC	864
	Pro	Lys	Gln	Arg	Gly	Met	Arg	Phe	Arg	Tyr	Lys	Cys	Glu	Gly	Arg	Ser	
			275					280					285				
15	GCG	GGC	AGC	ATC	CCA	GGC	GAG	AGG	AGC	ACA	GAT	ACC	ACC	AAG	ACC	CAC	912
	Ala	Gly	Ser	Ile	Pro	Gly	Glu	Arg	Ser	Thr	Asp	Thr	Thr	Lys	Thr	His	
		290					295					300					
20	CCC	ACC	ATC	AAG	ATC	AAT	GGC	TAC	ACA	GGA	CCA	GGG	ACA	GTG	CGC	ATC	960
	Pro	Thr	Ile	Lys	Ile	Asn	Gly	Tyr	Thr	Gly	Pro	Gly	Thr	Val	Arg	Ile	
	305					310					315					320	
25	TCC	CTG	GTC	ACC	AAG	GAC	CCT	CCT	CAC	CGG	CCT	CAC	CCC	CAC	GAG	CTT	1008
	Ser	Leu	Val	Thr	Lys	Asp	Pro	Pro	His	Arg	Pro	His	Pro	His	Glu	Leu	
					325					330					335		
30	GTA	GGA	AAG	GAC	TGC	CGG	GAT	GGC	TTC	TAT	GAG	GCT	GAG	CTC	TGC	CCG	1056
	Val	Gly	Lys	Asp	Cys	Arg	Asp	Gly	Phe	Tyr	Glu	Ala	Glu	Leu	Cys	Pro	
				340					345					350			
35	GAC	CGC	TGC	ATC	CAC	AGT	TTC	CAG	AAC	CTG	GGA	ATC	CAG	TGT	GTG	AAG	1104
	Asp	Arg	Cys	Ile	His	Ser	Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys	
			355					360					365				
	AAG	CGG	GAC	CTG	GAG	CAG	GCT	ATC	AGT	CAG	CGC	ATC	CAG	ACC	AAC	AAC	1152
	Lys	Arg	Asp	Leu	Glu	Gln	Ala	Ile	Ser	Gln	Arg	Ile	Gln	Thr	Asn	Asn	
			370				375					380					
40	AAC	CCC	TTC	CAA	GTT	CCT	ATA	GAA	GAG	CAG	CGT	GGG	GAC	TAC	GAC	CTG	1200
	Asn	Pro	Phe	Gln	Val	Pro	Ile	Glu	Glu	Gln	Arg	Gly	Asp	Tyr	Asp	Leu	
	385					390					395					400	
45	AAT	GCT	GTG	CGG	CTC	TGC	TTC	CAG	GTG	ACA	GTG	CGG	GAC	CCA	TCA	GGC	1248
	Asn	Ala	Val	Arg	Leu	Cys	Phe	Gln	Val	Thr	Val	Arg	Asp	Pro	Ser	Gly	
					405					410					415		
50	AGG	CCC	CTC	CGC	CTG	CCG	CCT	GTC	CTT	CCT	CAT	CCC	ATC	TTT	GAC	AAT	1296
	Arg	Pro	Leu	Arg	Leu	Pro	Pro	Val	Leu	Pro	His	Pro	Ile	Phe	Asp	Asn	
				420					425					430			
55	CGT	GCC	CCC	AAC	ACT	GCC	GAG	CTC	AAG	ATC	TGC	CGA	GTG	AAC	CGA	AAC	1344
	Arg	Ala	Pro	Asn	Thr	Ala	Glu	Leu	Lys	Ile	Cys	Arg	Val	Asn	Arg	Asn	
			435					440					445				
	TCT	GGC	AGC	TGC	CTC	GGT	GGG	GAT	GAG	ATC	TTC	CTA	CTG	TGT	GAC	AAG	1392

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	Ser	Gly	Ser	Cys	Leu	Gly	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	
	450					455					460						
5	GTG	CAG	AAA	GAG	GAC	ATT	GAG	GTG	TAT	TTC	ACG	GGA	CCA	GGC	TGG	GAG	1440
	Val	Gln	Lys	Glu	Asp	Ile	Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	
	465					470				475						480	
10	GCC	CGA	GGC	TCC	TTT	TCG	CAA	GCT	GAT	GTG	CAC	CGA	CAA	GTG	GCC	ATT	1488
	Ala	Arg	Gly	Ser	Phe	Ser	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	
					485					490					495		
15	GTG	TTC	CGG	ACC	CCT	CCC	TAC	GCA	GAC	CCC	AGC	CTG	CAG	GCT	CCT	GTG	1536
	Val	Phe	Arg	Thr	Pro	Pro	Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val	
				500					505					510			
	CGT	GTC	TCC	ATG	CAG	CTG	CGG	CGG	CCT	TCC	GAC	CGG	GAG	CTC	AGT	GAG	1584
	Arg	Val	Ser	Met	Gln	Leu	Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu	
			515					520					525				
20	CCC	ATG	GAA	TTC	CAG	TAC	CTG	CCA	GAT	ACA	GAC	GAT	CGT	CAC	CGG	ATT	1632
	Pro	Met	Glu	Phe	Gln	Tyr	Leu	Pro	Asp	Thr	Asp	Arg	Arg	His	Arg	Ile	
		530					535					540					
25	GAG	GAG	AAA	CGT	AAA	AGG	ACA	TAT	GAG	ACC	TTC	AAG	AGC	ATC	ATG	AAG	1680
	Glu	Glu	Lys	Arg	Lys	Arg	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	
	545					550					555					560	
30	AAG	AGT	CCT	TTC	AGC	GGA	CCC	ACC	GAC	CCC	CGG	CCT	CCA	CCT	CGA	CGC	1728
	Lys	Ser	Pro	Phe	Ser	Gly	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg	
					565					570					575		
35	ATT	GCT	GTG	CCT	TCC	CGC	AGC	TCA	GCT	TCT	GTC	CCC	AAG	CCA	GCA	CCC	1776
	Ile	Ala	Val	Pro	Ser	Arg	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	
				580					585						590		
	CAG	CCC	TAT	CCC	TTT	ACG	TCA	TCC	CTG	AGC	ACC	ATC	AAC	TAT	GAT	GAG	1824
	Gln	Pro	Tyr	Pro	Phe	Thr	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	
			595					600					605				
40	TTT	CCC	ACC	ATG	GTG	TTT	CCT	TCT	GGG	CAG	ATC	AGC	CAG	GCC	TCG	GCC	1872
	Phe	Pro	Thr	Met	Val	Phe	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	
		610					615					620					
45	TTG	GCC	CCG	GCC	CCT	CCC	CAA	GTC	CTG	CCC	CAG	GCT	CCA	GCC	CCT	GCC	1920
	Leu	Ala	Pro	Ala	Pro	Pro	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	
	625					630					635					640	
50	CCT	GCT	CCA	GCC	ATG	GTA	TCA	GCT	CTG	GCC	CAG	GCC	CCA	GCC	CCT	GTC	1968
	Pro	Ala	Pro	Ala	Met	Val	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	
					645					650					655		
55	CCA	GTC	CTA	GCC	CCA	GGC	CCT	CCT	CAG	GCT	GTG	GCC	CCA	CCT	GCC	CCC	2016
	Pro	Val	Leu	Ala	Pro	Gly	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	
				660					665						670		
	AAG	CCC	ACC	CAG	GCT	GGG	GAA	GGA	ACG	CTG	TCA	GAG	GCC	CTG	CTG	CAG	2064

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	Lys	Pro	Thr	Gln	Ala	Gly	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln					
							675									680				685	
5	CTG	CAG	TTT	GAT	GAT	GAA	GAC	CTG	GGG	GCC	TTG	CTT	GGC	AAC	AGC	ACA	2112				
	Leu	Gln	Phe	Asp	Asp	Glu	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr					
							690									695				700	
10	GAC	CCA	GCT	GTG	TTC	ACA	GAC	CTG	GCA	TCC	GTC	GAC	AAC	TCC	GAG	TTT	2160				
	Asp	Pro	Ala	Val	Phe	Thr	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe					
							705									710				715	720
15	CAG	CAG	CTG	CTG	AAC	CAG	GGC	ATA	CCT	GTG	GCC	CCC	CAC	ACA	ACT	GAG	2208				
	Gln	Gln	Leu	Leu	Asn	Gln	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu					
							725									730				735	
	CCC	ATG	CTG	ATG	GAG	TAC	CCT	GAG	GCT	ATA	ACT	CGC	CTA	GTG	ACA	GGG	2256				
	Pro	Met	Leu	Met	Glu	Tyr	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly					
							740									745				750	
20	GCC	CAG	AGG	CCC	CCC	GAC	CCA	GCT	CCT	GCT	CCA	CTG	GGG	GCC	CCG	GGG	2304				
	Ala	Gln	Arg	Pro	Pro	Asp	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly					
							755									760				765	
25	CTC	CCC	AAT	GGC	CTC	CTT	TCA	GGA	GAT	GAA	GAC	TTC	TCC	TCC	ATT	GCG	2352				
	Leu	Pro	Asn	Gly	Leu	Leu	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala					
							770									775				780	
30	GAC	ATG	GAC	TTC	TCA	GCC	CTG	CTG	AGT	CAG	ATC	AGC	TCC	TAA			2394				
	Asp	Met	Asp	Phe	Ser	Ala	Leu	Leu	Ser	Gln	Ile	Ser	Ser								
							785									790				795	

(2) INFORMATION FOR SEQ ID NO:143:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

45	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
	1				5					10					15	
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
				20					25					30		
50	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
			35					40					45			
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50						55					60				
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
55	65					70					75					80
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu

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				85				90				95				
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
				100					105					110		
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
5			115					120					125			
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
		130					135					140				
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
						150					155				160	
10	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
					165					170					175	
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
				180						185				190		
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
15			195					200					205			
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
		210					215					220				
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
		225				230					235				240	
20	Gly	Leu	Arg	Ser	Arg	Ala	Met	Asp	Glu	Leu	Phe	Pro	Leu	Ile	Phe	Pro
					245						250				255	
	Ala	Glu	Pro	Ala	Gln	Ala	Ser	Gly	Pro	Tyr	Val	Glu	Ile	Ile	Glu	Gln
			260						265					270		
	Pro	Lys	Gln	Arg	Gly	Met	Arg	Phe	Arg	Tyr	Lys	Cys	Glu	Gly	Arg	Ser
25			275					280					285			
	Ala	Gly	Ser	Ile	Pro	Gly	Glu	Arg	Ser	Thr	Asp	Thr	Thr	Lys	Thr	His
		290					295					300				
	Pro	Thr	Ile	Lys	Ile	Asn	Gly	Tyr	Thr	Gly	Pro	Gly	Thr	Val	Arg	Ile
		305				310					315				320	
30	Ser	Leu	Val	Thr	Lys	Asp	Pro	Pro	His	Arg	Pro	His	Pro	His	Glu	Leu
					325					330					335	
	Val	Gly	Lys	Asp	Cys	Arg	Asp	Gly	Phe	Tyr	Glu	Ala	Glu	Leu	Cys	Pro
			340						345					350		
	Asp	Arg	Cys	Ile	His	Ser	Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys
35			355					360					365			
	Lys	Arg	Asp	Leu	Glu	Gln	Ala	Ile	Ser	Gln	Arg	Ile	Gln	Thr	Asn	Asn
		370					375					380				
	Asn	Pro	Phe	Gln	Val	Pro	Ile	Glu	Glu	Gln	Arg	Gly	Asp	Tyr	Asp	Leu
		385				390					395				400	
40	Asn	Ala	Val	Arg	Leu	Cys	Phe	Gln	Val	Thr	Val	Arg	Asp	Pro	Ser	Gly
				405						410					415	
	Arg	Pro	Leu	Arg	Leu	Pro	Pro	Val	Leu	Pro	His	Pro	Ile	Phe	Asp	Asn
			420						425					430		
	Arg	Ala	Pro	Asn	Thr	Ala	Glu	Leu	Lys	Ile	Cys	Arg	Val	Asn	Arg	Asn
45			435					440					445			
	Ser	Gly	Ser	Cys	Leu	Gly	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys
		450					455					460				
	Val	Gln	Lys	Glu	Asp	Ile	Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu
		465				470					475				480	
50	Ala	Arg	Gly	Ser	Phe	Ser	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile
				485						490					495	
	Val	Phe	Arg	Thr	Pro	Pro	Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val
			500						505					510		
	Arg	Val	Ser	Met	Gln	Leu	Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu
55			515					520					525			
	Pro	Met	Glu	Phe	Gln	Tyr	Leu	Pro	Asp	Thr	Asp	Asp	Arg	His	Arg	Ile

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	530		535		540												
	Glu	Glu	Lys	Arg	Lys	Arg	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	
	545					550					555					560	
	Lys	Ser	Pro	Phe	Ser	Gly	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg	
5					565					570					575		
	Ile	Ala	Val	Pro	Ser	Arg	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	
				580					585					590			
	Gln	Pro	Tyr	Pro	Phe	Thr	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	
			595					600				605					
10	Phe	Pro	Thr	Met	Val	Phe	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	
	610						615					620					
	Leu	Ala	Pro	Ala	Pro	Pro	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	
	625					630					635				640		
	Pro	Ala	Pro	Ala	Met	Val	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	
15					645					650					655		
	Pro	Val	Leu	Ala	Pro	Gly	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	
				660					665				670				
	Lys	Pro	Thr	Gln	Ala	Gly	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	
			675					680				685					
20	Leu	Gln	Phe	Asp	Asp	Glu	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr	
	690						695					700					
	Asp	Pro	Ala	Val	Phe	Thr	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	
	705					710					715				720		
	Gln	Gln	Leu	Leu	Asn	Gln	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	
25					725					730					735		
	Pro	Met	Leu	Met	Glu	Tyr	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	
				740					745				750				
	Ala	Gln	Arg	Pro	Pro	Asp	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly	
			755				760					765					
30	Leu	Pro	Asn	Gly	Leu	Leu	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala	
	770						775				780						
	Asp	Met	Asp	Phe	Ser	Ala	Leu	Leu	Ser	Gln	Ile	Ser	Ser				
	785					790					795						

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CLAIMS

1. A method for extracting quantitative information relating to an influence on a cellular response, the method comprising recording variation, caused by the influence on a mechanically intact living cell or mechanically intact living cells, in spatially distributed light emitted from a luminophore, the luminophore being present in the cell or cells and being capable of being redistributed in a manner which is related with the degree of the influence, and/or of being modulated by a component which is capable of being redistributed in a manner which is related to the degree of the influence, the association resulting in a modulation of the luminescence characteristics of the luminophore, and processing the recorded variation in the spatially distributed light to provide quantitative information correlating the spatial distribution to the degree of the influence on the cellular response.
2. A method according to claim 1, as used for extracting quantitative information relating to an influence on an intracellular pathway involving redistribution of at least one component associated with the pathway, or part thereof, the method comprising recording the result of the influence on mechanically intact living cell or cells, as manifested in spatially distributed light emitted from a luminophore which is present in the cell or cells and which is capable of being redistributed, by modulation of the pathway, in a manner which is related to the redistribution of the at least one component of the intracellular pathway, processing the recorded result to provide quantitative information about the spatially distributed light and correlating the quantitative information to the degree of the influence on the intracellular pathway.
3. A method according to claim 1 or 2, wherein the quantitative information which is indicative of the degree of the cellular response to the influence or the result of the influence on the intracellular pathway is extracted from the recording or recordings according to a predetermined calibration based on responses or results, recorded in the same manner, to known degrees of a relevant specific influence.
4. A method according to any of the preceding claims, wherein the influence is contact between the mechanically intact living cell or the group of mechanically intact living cells with a

chemical substance and/or incubation of the mechanically intact living cell or the group of mechanically intact living cells with a chemical substance.

5 5. A method according to claim 4 wherein the substance is a substance whose effect on an intracellular pathway is to be determined.

6. A method according to any of the preceding claims, wherein the recording is made at a single point in time after the application of the influence.

10 7. A method according to any of claims 1-5, wherein the recording is made at two points in time, one point being before, and the other point being after the application of the influence.

15 8. A method according to any of claims 1-5, wherein the recording is performed at a series of points in time, in which the application of the influence occurs at some time after the first time point in the series of recordings, the recording being performed, e.g., with a predetermined time spacing of from 0.1 seconds to 1 hour, preferably from 1 to 60 seconds, more preferably from 1 to 30 seconds, in particular from 1 to 10 seconds, over a time span of from 1 second to 12 hours, such as from 10 seconds to 12 hours, e.g., from 10 seconds to one hour, such as from 60 seconds to 30 minutes or 20 minutes.

20

9. A method according to any of claims 1-7, wherein the cell or cells is/are fixed at a point in time after the application of the influence at which the response has been predetermined to be significant, and the recording is made at an arbitrary later time.

25 10. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of being redistributed in a manner which is physiologically relevant to the degree of the influence.

11. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of associating with a component which is capable of being redistributed in manner which is physiologically relevant to the degree of the influence.
- 5 12. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of being redistributed in a manner which is experimentally determined to be correlated to the degree of the influence.
- 10 13. A method according to any of the preceding claims, wherein the luminophore is a luminophore which is capable of being redistributed, by modulation of the intracellular pathway, in substantially the same manner as the at least one component of the intracellular pathway.
- 15 14. A method according to any of claims 1-13, wherein the luminophore is a luminophore which is capable of being quenched upon spatial association with a component which is redistributed by modulation of the pathway, the quenching being measured as a decrease in the intensity of the luminescence.
- 20 15. A method according to any of claims 1-13, wherein the variation or result with respect to the spatially distributed light emitted by the luminophore is detected by a change in the resonance energy transfer between the luminophore and another luminescent entity capable of delivering energy to the luminophore, each of which has been selected or engineered to become part of, bound to or associated with particular components of the intracellular pathway, and one of which undergoes redistribution in response to the influence, thereby changing the
- 25 amount of resonance energy transfer, the change in the resonance energy transfer being measured as a change in the intensity of emission from the luminophore.
- 30 16. A method according to claim 15, wherein the change in the intensity of the emission from the luminophore is sensed by a single channel photodetector which responds only to the average intensity of the luminophore in a non-spatially resolved fashion

17. A method according to any of claims 1-16, wherein the property of the light being recorded is intensity, fluorescence lifetime, polarization, wavelength shift, or other property which is modulated as a result of the underlying cellular response.

5

18. A method according to any of claims 1-15 or 17, wherein the recording of the spatially distributed light is performed using a recording system which records the spatial distribution of a recordable property of the light in the form of an ordered array of values.

10

19. A method according to claim 18, wherein the recording of the spatial distribution of the recordable property of the light is performed using a charge transfer device such as a CCD array or a vacuum tube device such as a vidicon tube.

15

20. A method according to any of the preceding claims, wherein the light to be measured passes through a filter which selects the desired component of the light to be measured and rejects other components.

21. A method according to any of the preceding claims, wherein the recording of the spatial distribution of the recordable property of light is performed by fluorescence microscopy.

20

22. A method according to any of the preceding claims, wherein the recording of the variation or result with respect to light emitted from the luminophore is performed by recording the spatially distributed light as one or more digital images, and the processing of the recorded variation to reduce it to one or more numbers representative of the degree of redistribution comprises a digital image processing procedure or combination of digital image processing procedures.

25

23. A method according to any of claims 2-22, wherein the intracellular pathway is an intracellular signalling pathway.

24. A method according to any of the preceding claims, wherein the luminophore is a fluorophore.
- 5 25. A method according to any of the preceding claims wherein the luminophore is a polypeptide encoded by and expressed from a nucleotide sequence harboured in the cell or cells.
- 10 26. A method according to any of the preceding claims, wherein the luminophore is a hybrid polypeptide comprising a fusion of at least a portion of each of two polypeptides one of which comprises a luminescent polypeptide and the other one of which comprises a biologically active polypeptide, as defined herein.
- 15 27. A method according to claim 26, wherein the luminescent polypeptide is a GFP as defined herein.
28. A method according to claim 27 wherein the GFP is selected from the group consisting of green fluorescent proteins having the F64L mutation as defined herein.
- 20 29. A method according to claim 28 wherein the GFP is a GFP variant selected from the group consisting of F64L-GFP, F64L-Y66H-GFP, F64L-S65T-GFP, and EGFP.
- 25 30. A method according to any of the previous claims for detecting intracellular translocation of a biologically active polypeptide affecting intracellular processes upon activation, the method comprising
- a) culturing one or more cells containing a nucleotide sequence coding for a hybrid polypeptide comprising a GFP which is N- or C-terminally tagged, optionally through a linker, to a biologically active polypeptide under conditions permitting expression of the nucleotide sequence,

- b) modulating the activity of the biologically active polypeptide by incubating the cell or cells with a substance having biological activity and
- c) measuring the fluorescence produced by the incubated cell or cells and determining the result or variation with respect to the fluorescence, such result or variation being
- 5 . indicative of the translocation of a biologically active polypeptide in said cell.

31. A method according to claim 30, wherein the nucleotide sequence is a DNA sequence.

32. A method according to claim 30 or 31, wherein the modulation is an activation.

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33. A method according to claim 30 or 31, wherein the modulation is a deactivation.

34. A method according to any of claims 30-33 wherein the fluorescence of the cell or cells is measured prior to the modulation, and the result or variation determined in step (c) is a

15 change in fluorescence compared to the fluorescence measured prior to the modulation.

35. A method according to any of claims 30-34, wherein the intracellular processes are intracellular signalling pathways.

20 36. A method according to claim 34, wherein the change in fluorescence measured in step (c) comprises determining a change in the spatial distribution of the fluorescence.

37. A method according to any of the preceding claims wherein the mechanically intact living cell or cells is/are a mammalian cell/mammalian cells which, during the time period over

25 which the influence is observed, is/are incubated at a temperature of 30°C or above, preferably at a temperature of from 32°C to 39°C, more preferably at a temperature of from 35°C to 38°C, and most preferably at a temperature of about 37°C.

38. A method according to any of the preceding claims, wherein the at least one mechanically intact living cell is part of a matrix of identical or non-identical cells.
39. A method according to any of claims 1-36 and 38, wherein the cell or cells is/are selected from the group consisting of fungal cells, such as a yeast cell; invertebrate cells including insect cells; and vertebrate cells, such as mammalian cells.
40. A nucleic acid construct coding for a fusion polypeptide comprising a biologically active polypeptide that is a component of an intracellular signalling pathway, or a part thereof, and a GFP, with the proviso that the construct is not a construct coding for a fusion polypeptide in which the biologically active polypeptide is selected from the group consisting of PKC-alpha, PKC-gamma, and PKC-epsilon.
41. A nucleic acid construct coding for a fusion polypeptide comprising a biologically active polypeptide that is a component of an intracellular signalling pathway, or a part thereof, and an F64L mutant of GFP.
42. A nucleic acid construct according to claim 40 or 41, wherein the biologically active polypeptide is a protein kinase or a phosphatase.
43. A nucleic acid construct according to any of claims 40-42 wherein the GFP is N- or C-terminally tagged, optionally via a peptide linker, to the biologically active polypeptide or part thereof.
44. A nucleic acid construct according to any of claims 40, 41 and 43, wherein the biologically active polypeptide is a transcription factor or a part thereof which changes cellular localisation upon activation.

45. A nucleic acid construct according to any of claims 40, 41 and 43, wherein the biologically active polypeptide is a protein, or a part thereof, which is associated with the cytoskeletal network and which changes cellular localisation upon activation.

- 5 46. A nucleic acid construct according to any of claims 40-43, wherein the biologically active polypeptide is a protein kinase or a part thereof which changes cellular localisation upon activation.

- 10 47. A nucleic acid construct according to claim 46, wherein the protein kinase is a serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.

48. A nucleic acid construct according to claim 46, wherein the protein kinase is a tyrosine protein kinase or a part thereof capable of changing intracellular localisation upon activation.

15

49. A nucleic acid construct according to claim 46, wherein the protein kinase is a phospholipid-dependent serine/threonine protein kinase or a part thereof capable of changing intracellular localisation upon activation.

- 20 50. A nucleic acid construct according to claim 46, wherein the protein kinase is a cAMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation.

- 25 51. A nucleic acid construct according to claim 50 which codes for a PKAc-F64L-S65T-GFP fusion.

52. A nucleic acid construct according to claim 46, wherein the protein kinase is a cGMP-dependent protein kinase or a part thereof capable of changing cellular localisation upon activation.

53. A nucleic acid construct according to claim 46, wherein the protein kinase is a calmodulin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

5

54. A nucleic acid construct according to claim 46, wherein the protein kinase is a mitogen-activated serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

10

55. A nucleic acid construct according to claim 54, which codes for an ERK1-F64L-S65T-GFP fusion.

56. A nucleic acid construct according to claim 54, which codes for an EGFP-ERK1 fusion.

15

57. A nucleic acid construct according to claim 46, wherein the protein kinase is a cyclin-dependent serine/threonine protein kinase or a part thereof capable of changing cellular localisation upon activation.

20

58. A nucleic acid construct according to claim 42 or 43, wherein the biologically active polypeptide is a protein phosphatase or a part thereof capable of changing cellular localisation upon activation.

59. A nucleic acid construct according to any of claims 40-58 which is a DNA construct.

25

60. A nucleic acid construct according to any of claims 40-59 wherein the gene encoding GFP is derived from *Aequorea victoria*.

61. A nucleic acid construct according to claim 60 in which the gene encoding GFP is the gene encoding EGFP as defined herein.

62. A nucleic acid construct according to claim 60 in which the gene encoding a GFP is a gene encoding a GFP variant selected from F64L-GFP, F64L-Y66H-GFP and F64L-S65T-GFP.

5

63. A DNA construct according to claim 59 and 61 or, where applicable, 62, which is a construct as identified by any of the DNA sequences shown in SEQ ID NO: 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, and 142, or is a variant thereof capable of encoding the same fusion polypeptide or a fusion polypeptide which is biologically equivalent thereto, as defined herein.

10

64. A cell containing a nucleic acid construct according to any of claims 40-63 and capable of expressing the sequence encoded by the construct.

15

65. A cell according to claim 64, which is a eukaryotic cell.

20

66. A cell according to claim 64, which is selected from the group consisting of fungal cells, such as yeast cells; invertebrate cells, including insect cells, and vertebrate cells, such as mammalian cells.

67. A cell according to claim 66, which is a mammalian cell.

25

68. An organism carrying in at least one of its component cells a nucleic acid sequence as contained in the constructs according to any of claims 40-59, said cell being capable of expressing said nucleic acid sequence.

69. An organism according to claim 68 which is selected from the group consisting of unicellular and multicellular organisms, such as a mammal.

70. A fluorescent probe comprising a GFP which is N- or C-terminally tagged, optionally via a peptide linker, to a biologically active polypeptide or a part or a subunit thereof which is a component of an intracellular signalling pathway as defined herein, the probe being a probe
5 which is encoded by the nucleic acid construct according to any of claims 40-59.

71. A method according to any of claims 1-39, wherein the luminophore is a fusion polypeptide as encoded by the nucleic acid construct according to any of claims 40-63.

10 72. A method according to any of claims 1-39 or 71 in which the method of the invention is used in a screening program as defined herein.

73. An apparatus for measuring the distribution of fluorescence in at least one cell, and thereby any change in the distribution of fluorescence in at least one cell, which includes the
15 following component parts: (a) a light source, (b) a means for selecting the wavelength(s) of light from the source which will excite the fluorescence of the protein, (c) a means for rapidly blocking or passing the excitation light into the rest of the system, (d) a series of optical elements for conveying the excitation light to the specimen, collecting the emitted fluorescence in a spatially resolved fashion, and forming an image from this fluorescence, (e) a
20 bench or stand which holds the container of the cells being measured in a predetermined geometry with respect to the series of optical elements, (f) a detector to record the spatially resolved fluorescence in the form of an image, (g) a computer or electronic system and associated software to acquire and store the recorded images, and to compute the degree of redistribution from the recorded images.

25

74. An apparatus according to claim 73 in which some or all of the system is automated.

75. An apparatus according to claim 73 in which components d and e comprise a fluorescence microscope.

30

76. An apparatus according to claim 73 in which component f is a CCD camera.

77. An apparatus according to claim 73 in which the image is formed and recorded by an optical scanning system.

5

78. An apparatus according to claim 73 in which a liquid addition system is used to add a known or unknown compound to any or all of the cells in the cell holder at a time determined in advance.

10 79. An apparatus according to claim 78 in which the liquid addition system is under the control of the computer or electronic system.

15 80. A method according to any of claims 1-79 wherein the method is a screening program for the identification of a biologically active substance as defined herein that directly or indirectly affects an intracellular signalling pathway and is potentially useful as a medicament, wherein the result of the individual measurement of each substance being screened which indicates its potential biological activity is based on measurement of the redistribution of spatially resolved luminescence in living cells and which undergoes a change in distribution upon activation of an intracellular signalling pathway.

20

25 81 A method according to any of claims 1-79 wherein the method is a screening program for the identification of a biologically toxic substance as defined herein that exerts its toxic effect by interfering with an intracellular signalling pathway, wherein the result of the individual measurement of each substance being screened which indicates its potential biologically toxic activity is based on measurement of the redistribution of said fluorescent probe in living cells and which undergoes a change in distribution upon activation of an intracellular signalling pathway.

30 82. A method according to any of claims 1-80 wherein a fluorescent probe is used in back-tracking of signal transduction pathways as defined herein.

83. A method of treating a condition or disease related to the intracellular function of a protein kinase comprising administering to a patient suffering from said condition or disease an effective amount of a compound which has been discovered by any method according to the invention.

84. A compound that modulates a component of an intracellular pathway as defined herein, as determined by a method according to the method of the invention.

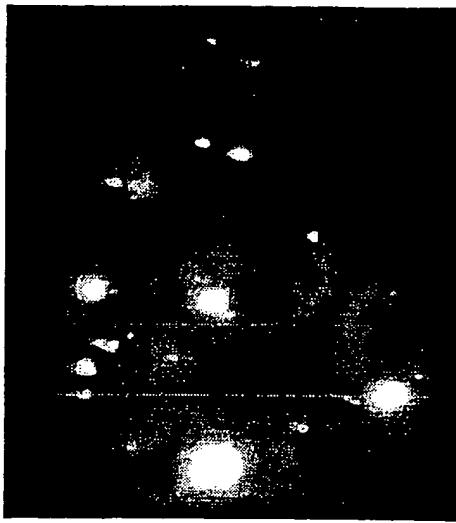
85. A medical composition comprising a therapeutic amount of a compound identified according to the method of the invention.

86. A method of selectively treating a patient suffering from an ailment which responds to medical treatment comprising obtaining a primary cell or cells from said patient, transfecting the cell or cells with at least one DNA sequence encoding a fluorescent probe according to the invention, culturing the cell or cells under conditions permitting the expression of said probes and exposing it to an array of medicaments suspected of being capable of alleviating said ailment, then comparing changes in fluorescence patterns or redistribution patterns of the fluorescent probes in the intact living cell or cells to detect the cellular response to the specific medicaments (obtaining a cellular action profile), then selecting a medicament(s) based on desired activity and acceptable level of side effects and administering an effective amount of said medicament(s) to said patient.

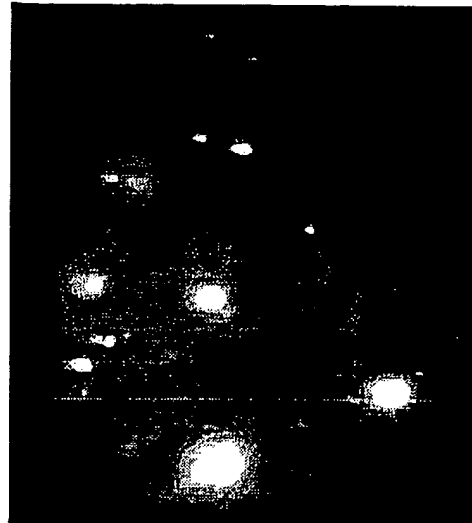
87. A method according to any of claims 1-80 of identifying a drug target among the group of biologically active polypeptides which are components of intracellular signalling pathways.

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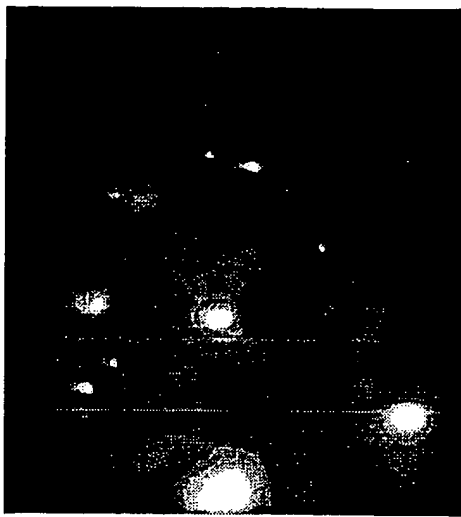
Fig 1



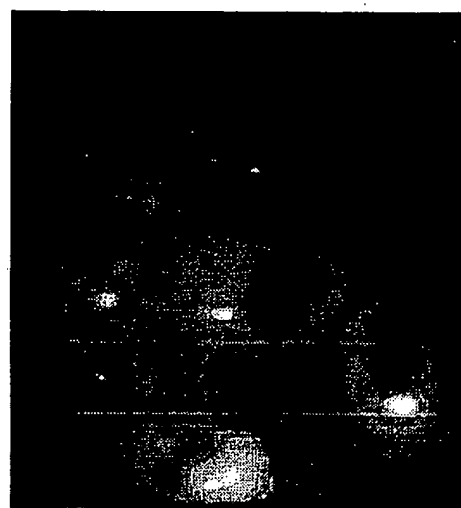
a)



b)



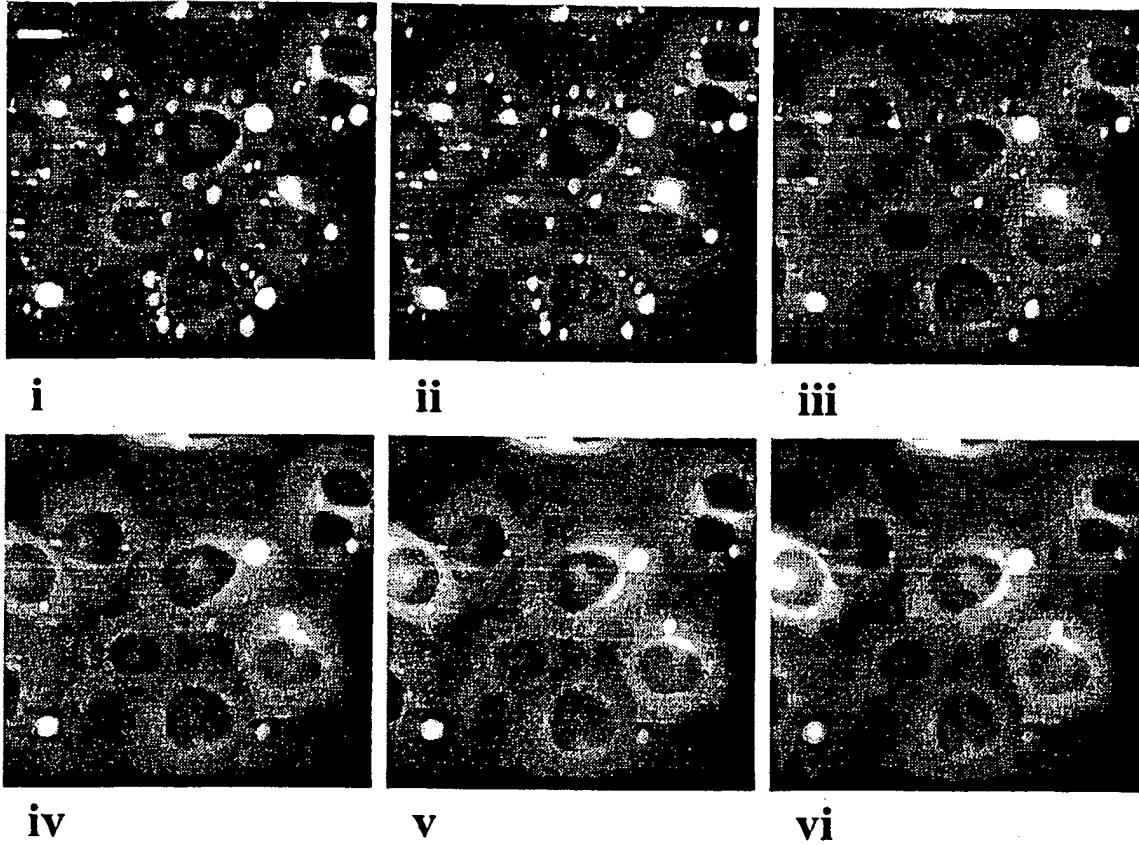
c)



d)

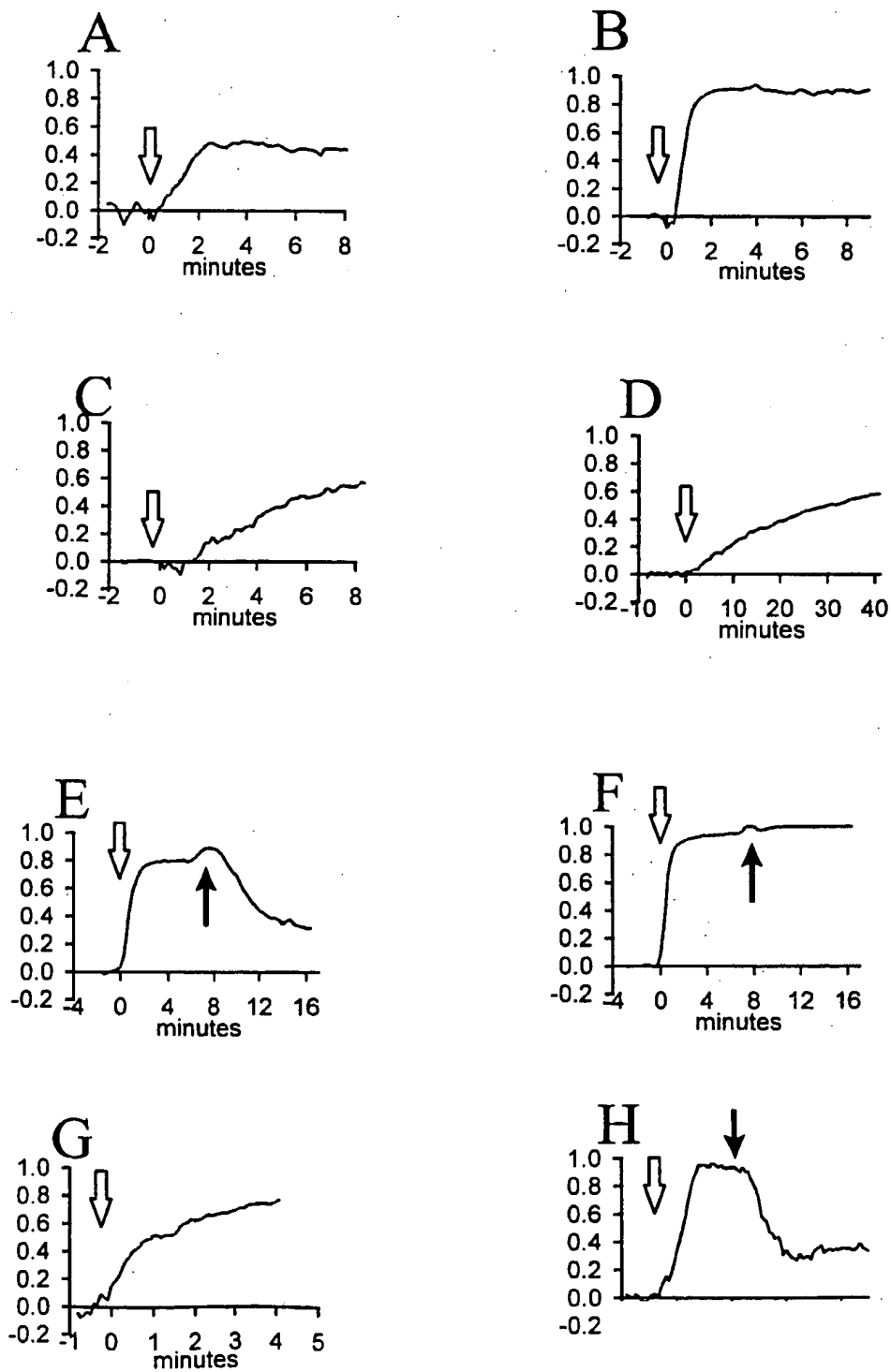
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Fig 2



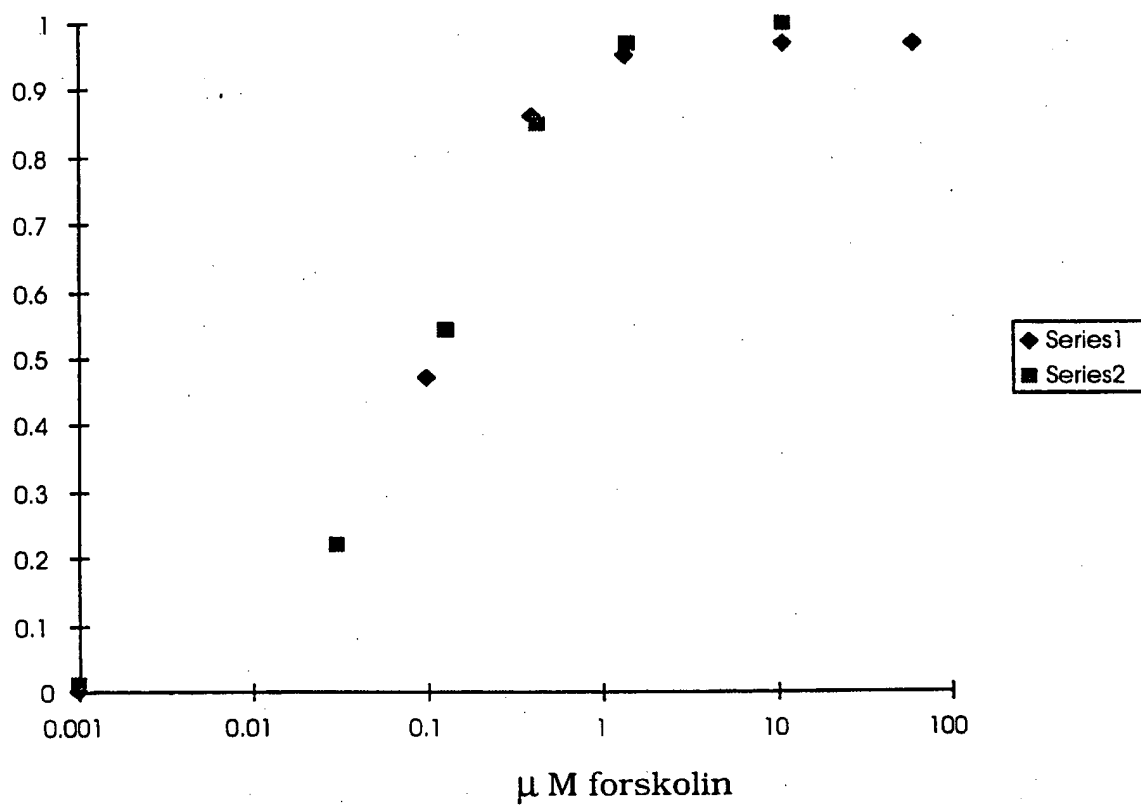
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Fig 3



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Fig 4



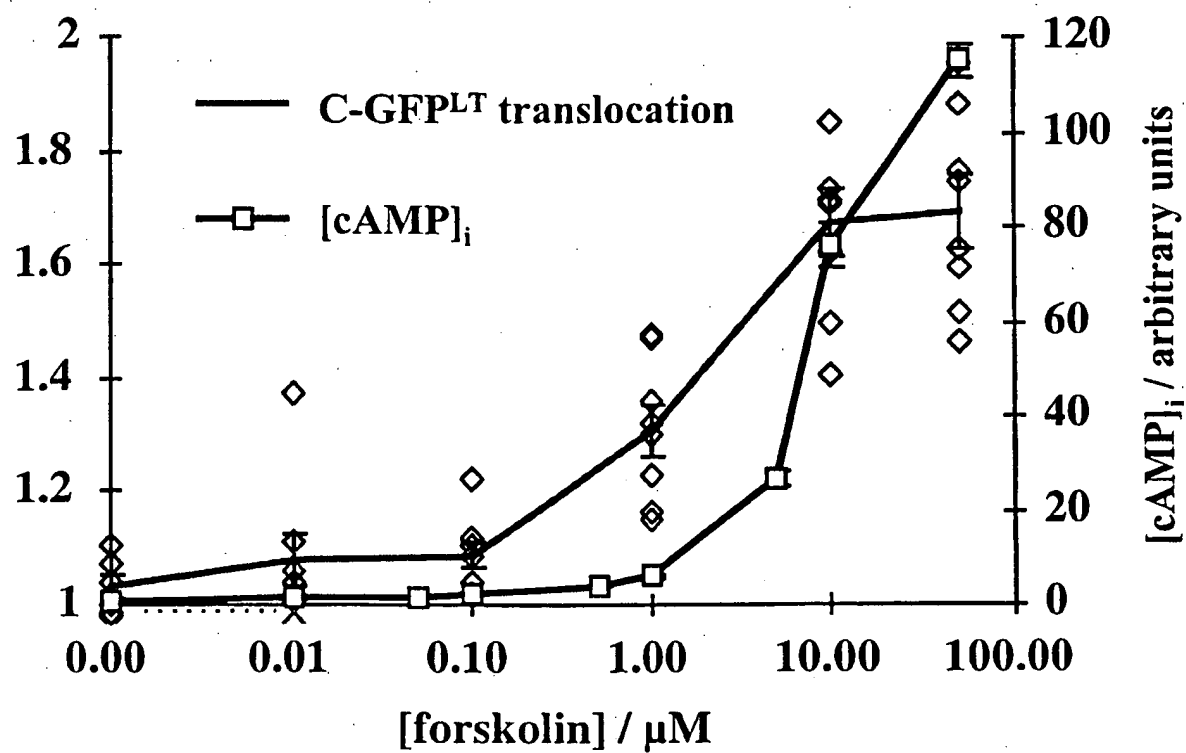
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Fig 5

[forskolin] μ M	$t_{1/2\max}$ / s	t_{\max} / s
1	115 \pm 21	310 \pm 31
10	69 \pm 14	224 \pm 47
50	47 \pm 10	125 \pm 28

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Fig 6

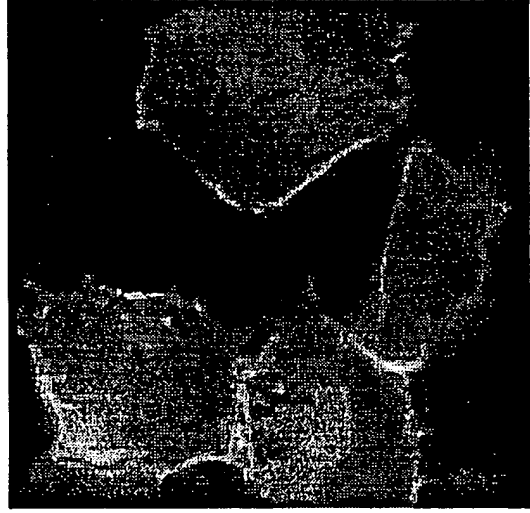


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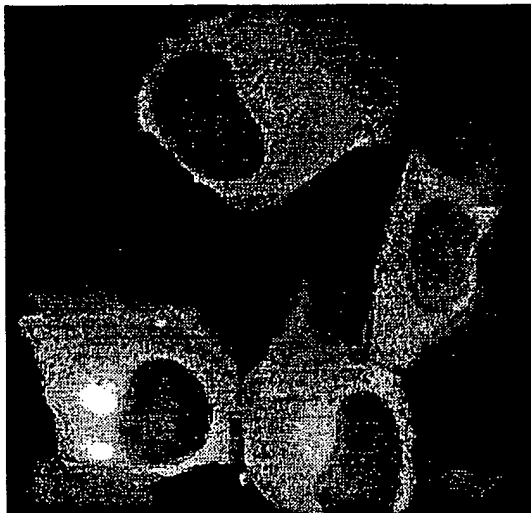
Fig 7



a)



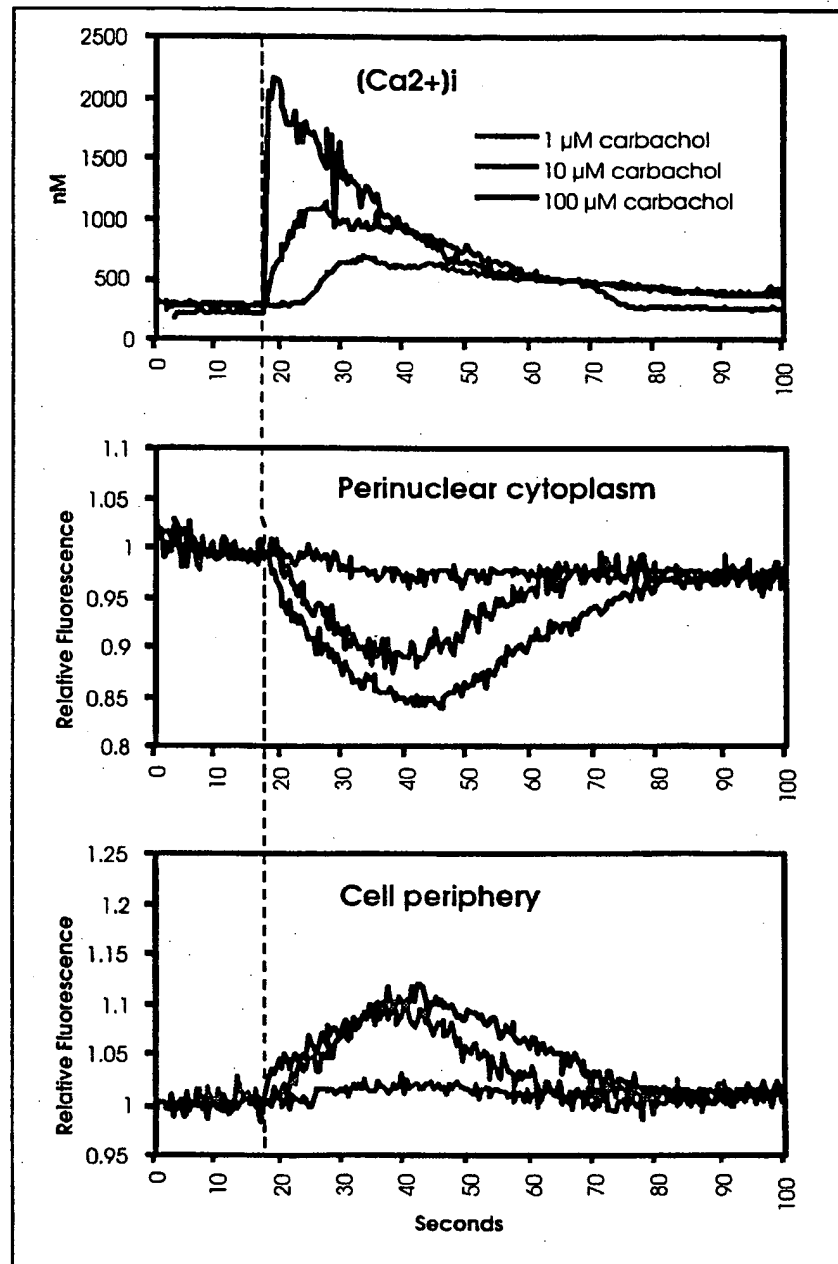
b)



c)

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Fig 8



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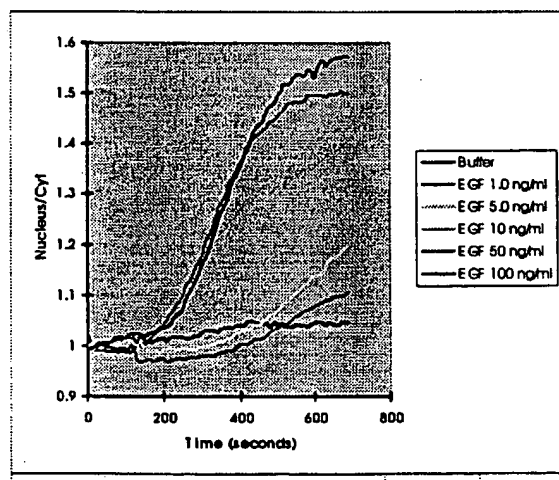
Fig 9



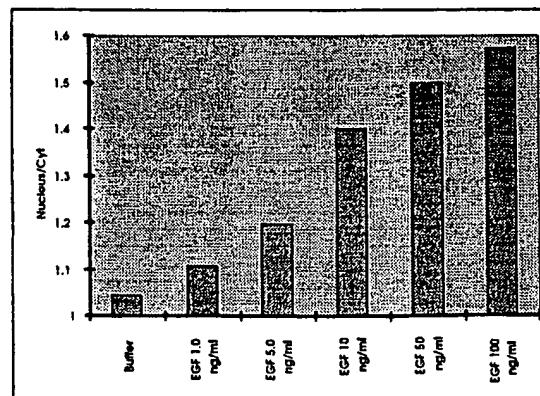
a)



b)



c)

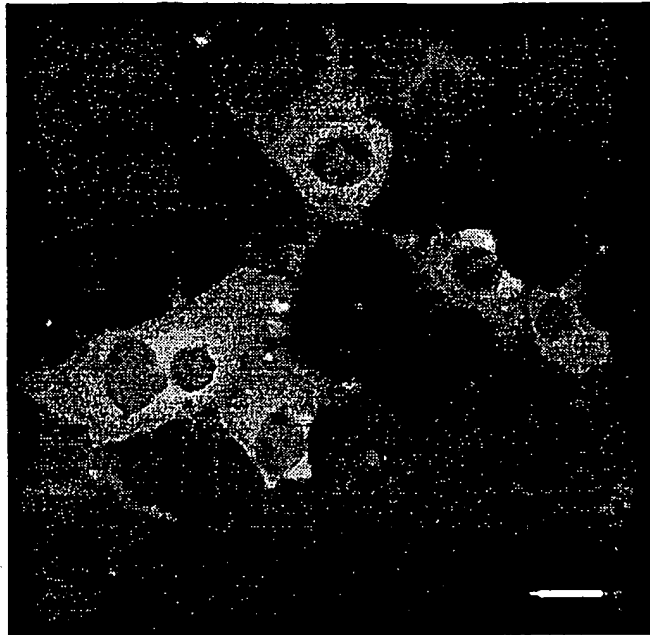


d)

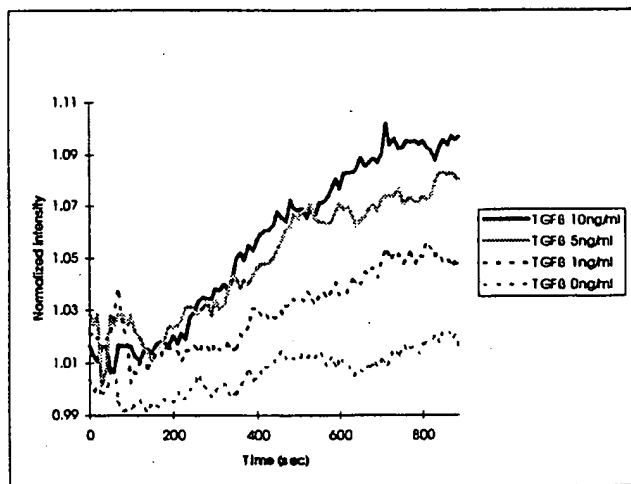
10 /12

Fig 10

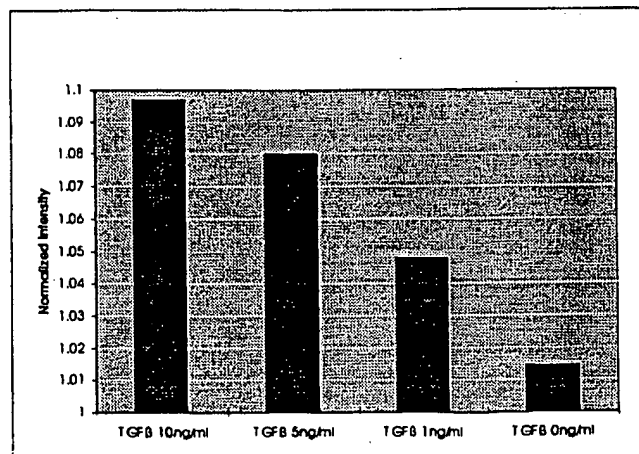
a)



b)

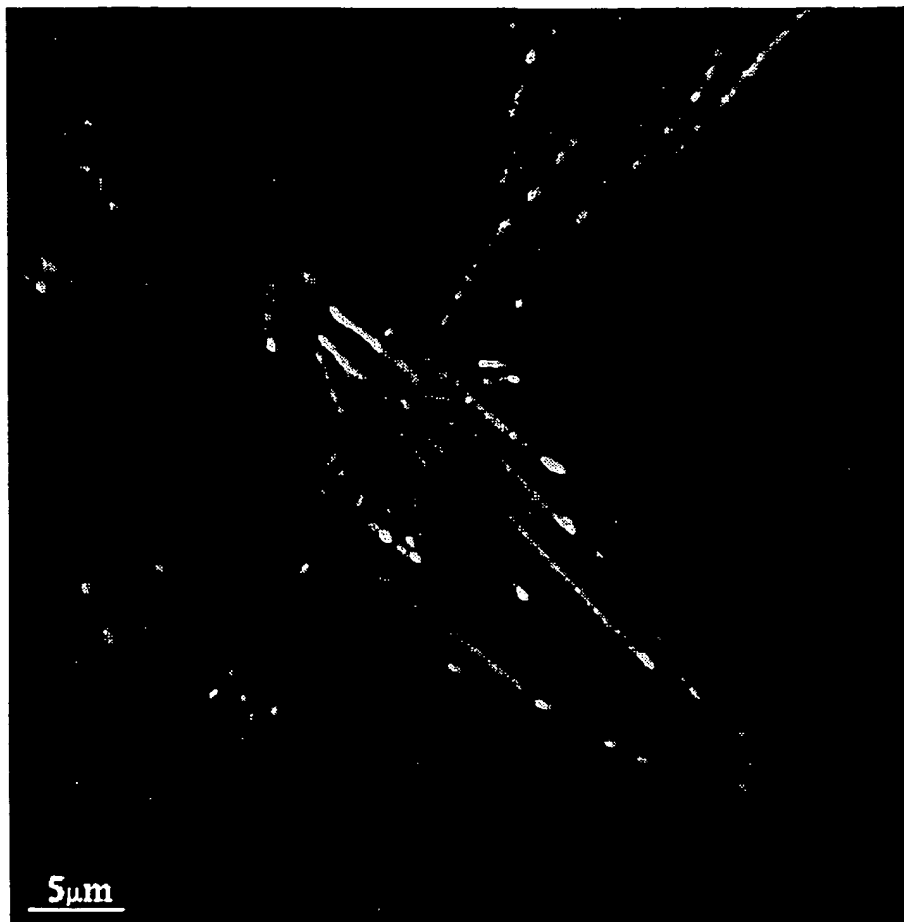


c)



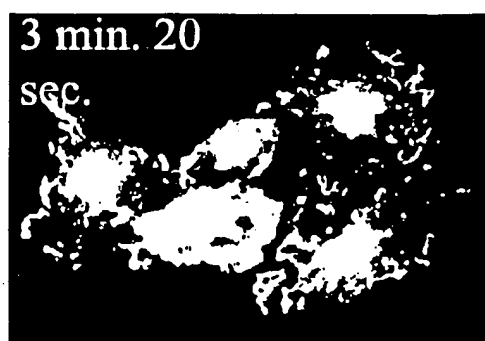
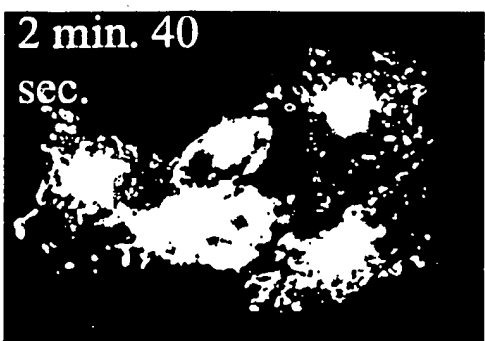
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Fig 11



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Fig. 12





INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : G01N 33/50, C12Q 1/48, 1/25	A3	(11) International Publication Number: WO 98/45704 (43) International Publication Date: 15 October 1998 (15.10.98)
<p>(21) International Application Number: PCT/DK98/00145</p> <p>(22) International Filing Date: 7 April 1998 (07.04.98)</p> <p>(30) Priority Data: 0392/97 7 April 1997 (07.04.97) DK</p> <p>(71) Applicant (for all designated States except US): NOVO NORDISK A/S [DK/DK]; Novo Allé, DK-2880 Bagsvaerd (DK).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): THASTRUP, Ole [DK/DK]; Birkevej 37, DK-3460 Birkerød (DK). PETERSEN BJØRN, Sara [DK/DK]; Klampenborgvej 102, DK-2800 Lyngby (DK). TULLIN, Søren [DK/DK]; Karl Gjellerups Alle 18, DK-2860 Søborg (DK). KASPER, Almholt [DK/DK]; Eigilsgade 32, 4. tv, DK-2300 København S (DK). SCUDDER, Kurt [US/DK]; Lavendelhaven 70, DK-2830 Virum (DK).</p> <p>(74) Common Representative: NOVO NORDISK A/S; attn. Lars Kellberg, Novo Allé, DK-2880 Bagsværd (DK).</p>	<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p> <p>(88) Date of publication of the international search report: 22 April 1999 (22.04.99)</p>	
<p>(54) Title: A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE</p>		
<p>(57) Abstract</p> <p>Cells are genetically modified to express a luminophore, e.g., a modified (F64L, S65T, Y66H) Green Fluorescent Protein (GFP, EGFP) coupled to a component of an intracellular signalling pathway such as a transcription factor, a cGMP- or cAMP-dependent protein kinase, a cyclin-, calmodulin- or phospholipid-dependent or mitogen-activated serine/threonine protein kinase, a tyrosine protein kinase, or a protein phosphatase (e.g. PKA, PKC, Erk, Smad, VASP, actin, p38, Jnk1, PKG, IkappaB, CDK2, Grk5, Zap70, p85, protein-tyrosine phosphatase 1C, Stat5, NFAT, NFkappaB, RhoA, PKB). An influence modulates the intracellular signalling pathway in such a way that the luminophore is being redistributed or translocated with the component in living cells in a manner experimentally determined to be correlated to the degree of the influence. Measurement of redistribution is performed by recording of light intensity, fluorescence lifetime, polarization, wavelength shift, resonance energy transfer, or other properties by an apparatus consisting of e.g. a fluorescence microscope and a CCD camera. Data stored as digital images are processed to numbers representing the degree of redistribution. The method can be used as a screening program for identifying a compound that modulates a component and is capable of treating a disease related to the function of the component.</p>		

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INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/DK 98/00145

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 G01N33/50 C12Q1/48 C12Q1/25

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 G01N C12Q C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 11094 A (NOVONORDISK AS ;THASTRUP OLE (DK); TULLIN SOEREN (DK); POULSEN LAR) 27 March 1997	1-27, 30-40, 44-60, 64-82,88
Y	see the whole document see claims	28,29, 41,61-63
X	WO 91 01305 A (UNIV WALES MEDICINE) 7 February 1991	1-27, 30-40, 42-60, 64-84, 87,88
Y	see page 4, line 15 - line 20 see claims see examples 1-10	28,29, 41,61-63



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

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Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

Int. Application No

PCT/DK 98/00145

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 07463 A (UNIV COLUMBIA ; WOODS HOLE OCEANOGRAPHIC INST (US); CHALFIE MARTIN) 16 March 1995 cited in the application	1-27, 30-40, 42-60, 64-84, 87, 88
Y	see claim 26 see the whole document	28, 29, 41, 61-63
Y	WO 96 23898 A (NOVONORDISK AS ; THASTRUP OLE (DK); TULLIN SOEREN (DK); POULSEN LAR) 8 August 1996 see the whole document	28, 29, 41, 61-63
X	see page 8-17	42, 43, 46, 47
X	WO 96 03649 A (UNIV NORTH CAROLINA) 8 February 1996 see page 49; example 6.10	45
P, X	WO 97 20931 A (US HEALTH ; HTUN HAN (US); HAGER GORDON L (US)) 12 June 1997 see claims 41-58	40, 44
P, X	WO 97 30074 A (CYTOGEN CORP ; UNIV NORTH CAROLINA (US)) 21 August 1997 see page 57	44
P, X	WO 98 02571 A (TSIEN ROGER Y ; CUBITT ANDREW B (US); UNIV CALIFORNIA (US)) 22 January 1998 see claims	1-27, 30-40, 42-50, 52-54, 57-60, 64-82, 88
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C.(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication where appropriate, of the relevant passages	Relevant to claim No.
P,X	SAKAI, N. ET AL.: "Direct visualization of the translocation of the gamma subspecies of protein kinase c in living cells using fusion proteins with green fluorescent protein." THE JOURNAL OF CELL BIOLOGY, vol. 139, no. 6, 15 December 1997, pages 1465-1476, XP002078902 see the whole document	1-43,46, 47,49, 53-57, 59-82,88
O,X	& Direct visualization of the translocation of the gamma subspecies of protein kinase c in living cells using fusion proteins with green fluorescent protein.Meeting held at 22-23.03.97 cited in the application see abstract	
X	--- SCHMIDT, D.J. ET AL.: "Dynamic analysis of alpha-PKC-GFP chimera translocation events in smooth muscle with ultra-high speed 3D fluorescence microscopy" FASEB JOURNAL, vol. 11, no. 3, 28 February 1997, page A505 XP002077257 cited in the application see abstract	1-43,46, 47,49, 53-57, 59-82,88
X	--- GERISCH, GUENTHER ET AL: "Chemoattractant-controlled accumulation of coronin at the leading edge of Dictyostelium cells monitored using a green fluorescent protein-coronin fusion protein" CURR. BIOL. (1995), 5(11), 1280-5 CODEN: CUBLE2;ISSN: 0960-9822, XP002089510 see abstract p 1281, right col, second full , last sentence	1,40,43, 45
X	--- SIDOROVA, JULIA M. ET AL: "Cell cycle-regulated phosphorylation of Swi6 controls its nuclear localization" MOL. BIOL. CELL (1995), 6(12), 1641-58 CODEN: MBCEEV;ISSN: 1059-1524, XP002089512 see the whole document	40,43,44
X	--- HAN HTUN ET AL: "VISUALIZATION OF GLUCOCORTICOID RECEPTOR TRANSLOCATION AND INTRANUCLEAR ORGANIZATION IN LIVING CELLS WITH A GREEN FLUORESCENT PROTEIN CHIMERA" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 93, no. 10, May 1996, pages 4845-4850, XP002029560 see the whole document	1-40,44, 64-72
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Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CAREY K L ET AL: "EVIDENCE USING A GREEN FLUORESCENT PROTEIN-GLUCOCORTICOID RECEPTOR CHIMERA THAT THE RAN/TC4 GTPASE MEDIATES AN ESSENTIAL FUNCTION INDEPENDENT OF NUCLEAR PROTEIN IMPORT" THE JOURNAL OF CELL BIOLOGY, vol. 133, no. 5, June 1996, pages 985-996, XP000670316 cited in the application see the whole document ---	1-40,44, 64-72
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 98/00145

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 83-84 and claim 87 relate to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition (Rule 39.1(iv) PCT - Method for treatment of the human or animal body by therapy).
2. ☒ Claims Nos.: 85,86
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Claims Nos.: 85,86

The subject-matter (compounds per se) is solely characterised in claims 85 and 86 by the result to be achieved, no support of a technical character is derivable from the description for the technical formulation of the subject of the search, accordingly no scope of a search could be defined and a meaningful search is hence not possible.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Partially: 1-43, 46, 59-82 and 88; Entirely: 47, 49, 53-57

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being serine/threonine protein kinases

2. Claims: Partially: 1-41, 43, 59-82 and 88; Entirely: 48

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being tyrosine kinases

3. Claims: Partially: 1-43, 46, 59-82 and 88; Entirely: 50, 51

MMethods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being cAMP dependent protein kinases.

4. Claims: Partially: 1-43, 46, 59-82 and 88; Entirely: 52

MMethods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being cGMP dependent protein kinases

5. Claims: Partially: 1-43, 59-82 and 88; Entirely: 58

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being protein phosphatases

6. Claims: Partially: 1-41, 43, 59-82 and 88; Entirely: 44

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being transcription factors

7. Claims: Partially: 1-41, 43, 59-82 and 88; Entirely: 45

Methods for extracting information from influences on a living cell involving observing spatial redistribution or modulation of a luminophore linked to a biologically active molecule, in particular to a molecule involved in intracellular signalling pathways, nucleic acids encoding fusion proteins comprising both the luminophore and the biological active molecule, cells containing and expressing these nucleic acids, as well as methods and apparatuses involving above products, in so far as related to the biologically active protein being proteins associated with the cytoskeletal network

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/DK 98/00145

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